

DR 11101: LAW 92796.

49 How Bt protein regulates cell death and cell survival pathways
50 downstreams, RNA and antibodies also regulate intracellular
51 activation for treated ATR cancer
52
53 Summary: Fig 6B, Supp. Material
54
55 Bt protein regulates the activation of a novel human B1 protein which
56 can interact with intracellular mediators or modulators of inflammation,
57 cell death and/or cell survival pathways, downstream indirectly, leads
58 can be mediated or mediated in inflammation, cell death or cell survival
59 pathways and/or intracellular signalling activity using B1.
60 Conditioners such as ATR and cancer can be treated using B1. Antibodies,
61 compounds, drugs and enzymes can also be used to regulate the above
62 pathway.
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Abstracts associated with increased PMSI expression/activity. PRSP
antagonists are useful for treating or preventing disorders associated
with increased PMSI expression/activity.

Schneider, 2004; PD, 61d A, 41f C, 47 G, 53 L; 3 others

QY 58 g|c aqcl |stgt |cqqat aacatc qac|qclq|lqqc |al |cqqaaat qqqccccc 117
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 Db | |c|cagcl |ccl |cqaagaaacacgccl |ccctq|qacat |ccqaaal |qqccccc 60

QY 118 ataacctgactgttgcacccggaagaaagatcttaccgactctctctctctcgaaggaagatctc 177
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DB 61 ataacctgactgttgcacccggaagaaagatcttaccgactctctctctcgaaggaagatctc 120

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Q7	219	297
nl	181	24

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RESULT 2
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ID AAZ46141 standard, cDNA, 2021 BP.
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AC AAZ46141,
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ID 16-MAY-2000 (first entry)
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DE cDNA sequence encoding a human phosphorylation effector PHSP-6.
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KW Human, phosphorylation effector, PHCT, proliferative disorder,
KW Immune disorder; neuronal disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FI CDS 231..1825
FI /fla a
FI /product "phosphorylation effector"
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FN W020004728-A2.
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PD 10-FEB-2000
XX
FI 28-MAR-1999 98US-018171A2.
XX
FI 28-MAR-1999 98US-012345A.
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FI 14-SEP-1999 98US-015281A.
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FI 14-OCT-1998 98US-017348A2.
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FI 03-NOV-1998 98US-0106889.
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FI 19-NOV-1998 98US-010409A.
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FI 22-DEC-1998 98US-0113796.
XX
FI 12-JAN-1999 99US-017345A.
XX
FI 12-JAN-1999 99US-022900A.
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LA (INCYT) INCYTE PHARM INC.
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PI Hillman JL, Lal P, Tang YL, Corley NB, Guebler KJ, Baughn MK;
PI Patterson S, Bandman D, Ah-Young I, Gorgone CA, Yoo H, Azimati Y,
PI Reddy R, Lu DAM, Shah LL;
XX
WI WI, 2000-183125/16.
XX
FI FIDB: AAZ-8774.
XX
PT New human phosphorylation effectors use of for the diagnosis, treatment
PI and prevention of proliferative, immune and neuronal disorders.
XX
PS Claim 1, Page 121-122; 142pp; English.
XX
CC AAZ46141 246168 encode human phosphorylation effectors (PHSP),
CC designated PHSP1 PHSP31 (the protein sequence for PHSP2P is not given
CC in the specification). The sequences were isolated from cDNA libraries
CC prepared from various human tissues. The PHSP proteins are useful for
CC the diagnosis, treatment and prevention of proliferative disorders,
CC immune disorders and neuronal disorders. The PHSP proteins form
CC pharmaceutical compositions which useful for treating or preventing

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2. *Chlorophyll a* and *Chlorophyll b* contents were determined by spectrophotometry using the method of Lichtenthaler and Whistler (1987).

Query Match: 78.8%; Score: 1654; DB: z1; Length: 2709;
 Best Local Similarity: 99.7%; Pred. Neg. 0;
 Matches: 1954; Conservative: 0; Mismatches: 6; Indels: 0; Gaps:

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 QY 140 aaagggttcttgcggccctcgtcgtgcaggaggttatctggggccctcgtgcaggaggttg 199
 Db 147 aaagggttcttgcggccctcgtcgtgcaggaggttatctggggccctcgtgcaggaggttg 206
 QY 200 gacaccttggggccggcggcaggaggggacacacgggacacacgggacacacgggacac 259
 Db 207 gacaccttggggccggcggcaggaggggacacacgggacacacgggacacacgggacac 266
 QY 260 atgaaaggggaggagacatctgcaggccctgcggacacattccctacacacacacacac 319
 Db 267 atgaaaggggaggagacatctgcaggccctgcggacacattccctacacacacacacac 326
 QY 320 ctgcgcctac 379
 Db 327 ctgcgcctac 386
 QY 380 cgcctcagagtgagggttgaagacacacacacacacacacacacacacacacacacac 439
 Db 387 cgcctcagagtgagggttgaagacacacacacacacacacacacacacacacacacac 446
 QY 440 aaggatgttttaagagaaagctgaaattttacacaaagctgagatttaattacatttttcca 499
 Db 447 aaggatgttttaagagaaagctgaaattttacacaaagctgagatttaattacatttttcca 506
 QY 500 attttgggaattttgcaatgagcctgaattttttgggaatagttactgaatcacatgcacaa 559
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 QY 620 agatttcgcac 679
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 QY 680 cctttacttcaac 739
 Db 687 cctttacttcaac 746
 QY 740 aagatctgcagatttttggtttatcaaaagtgggccatgatgcctctctcacagtcacgaag 799
 Db 747 aagatctgcagatttttggtttatcaaaagtgggccatgatgcctctctcacagtcacgaag 806
 QY 800 aggaac 859
 Db 807 aggaac 866
 QY 860 ggaac 919
 Db 867 ggaac 926
 QY 920 aggaac 979
 Db 927 aggaac 986
 QY 980 agtctgtgcac 1039
 Db 987 agtctgtgcac 1046
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QY 1160 acctttcttcaaaatgtttaaatagaacttgaacacagtttttgagacacatttgaagagata 1219
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 Db 1287 caac 1346
 QY 1340 caac 1399
 Db 1347 caac 1406
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 Db 1407 tattttatgaac 1466
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 QY 1520 caac 1579
 Db 1527 caac 1586
 QY 1580 caac 1639
 Db 1587 caac 1646
 QY 1640 gatgcctctctctcaac 1699
 Db 1647 gatgcctctctctcaac 1706
 QY 1700 caac 1759
 Db 1707 caac 1766
 QY 1760 ttttcaac 1819
 Db 1767 ttttcaac 1826
 QY 1820 caac 1879
 Db 1827 caac 1886
 QY 1880 caac 1939
 Db 1887 caac 1946
 QY 1940 ttttcaac 1979
 Db 1947 ttttcaac 1986

RESULT 4

AAK94554

ID AAK94554 standard; cDNA; 2033 BP.

XX

AC AAK94554;

XX

ET 06 Nov 2001 (first entry)

XX

DE Human full-length cDNA, SEQ ID NO: 3453.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX

OS Homo sapiens.

XX

PN EP110094-A2.

XX

IR (KBr): ν_{max} 3440 (broad), 2950, 1640, 1540, 1450, 1380, 1270, 1140, 1040, 1010, 960, 910, 860, 820, 760, 720, 690, 650, 610, 570, 530, 500, 470, 440, 410, 380, 350, 320, 300, 270, 240, 210, 180, 150, 120, 90, 60, 30, 0.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 104

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RESIDU 6
AAF0001:
ID AAF0001 standard: rDNA, 1941 bp.
XX
AC AAF0001:
XX
ID 23-ApR-2001 (first entry)
XX
DE Human CARD-3 rDNA.
XX
KW CARD-3; caspase recruitment domain; human; cancer; infection;
KW autoimmune disease; neurological disease; hematological disease;
KW immune disease; inflammation; antitumor; antiseptic;
KW immunomodulator; antiinflammatory; apoptosis; diagnosis;
KW gene therapy; ss
XX
OS Homo sapiens.
XX
FH Key: 1000000/Qualifiers
FR CHS 214, 1826
FI Z/Strain: a
FI Z/note: "the open reading frame is also specifically
FI claimed in claim 1(a)"
XX
FN W0200100825_A2
XX
ID 04-JAN-2001.
XX
ID 28-JUN-2000, 2000W030817191.
XX
ID 28-JUN-1999, 19990344020.
XX
ID (BRIEF) SEQUENCE CHARACTERISTICS
XX
ID Berlin 1:
XX
ID W01, 2001061974/37.
ID F:PSDB: AAB20079.
XX
ID Isolated intracellular proteins produced to be involved in regulating
ID caspase activation are used for diagnosis and treatment of e.g. cancer
ID viral infections, autoimmune diseases, neurological diseases and
ID hematological disorders
XX
OS Strain 1(a), Fig 1: 208pp; English
XX
ID The present sequence is that of rDNA encoding human caspase
ID recruitment domain 3 (CARD-3, see AAB20079). The rDNA was isolated
ID following a database search using known CARD sequences. Plasmid

```

CC pXFL7A containing CARD-3 cDNA is deposited as ATCC 233037. CARD-3
 CC is an intracellular protein predicted to be involved in regulating
 CC caspase activation. It is useful as a modulating agent in
 CC regulating cellular processes include cell growth and cell death.
 CC Methods of diagnosing and treating patients suffering from a
 CC disorder associated with an abnormal level or rate of apoptotic
 CC cell death, abnormal activity of the Fas /FasL receptor complex,
 CC abnormal activity of the tumour necrosis factor receptor complex
 CC or abnormal activity of a caspase involve administering a compound
 CC that modulates the expression or activity of CARD-3, CARD-4, CARD-5
 CC or CARD-6, a small molecule, antisense molecule, siRNA, ribozyme
 CC or polypeptide. Such disorders include cancer, viral infection,
 CC autoimmune disorders, neurological diseases, haematological
 CC disorders, inflammatory disorders and immune disorders. CARD
 CC nucleic acids can be used to express CARD proteins in a host cell
 CC e.g. for gene therapy applications, to detect a genetic lesion and
 CC to modulate CARD activity.

CC XX
 CC SQ Sequence 1931 BP; 614 A; 428 C; 416 G; 474 T; 3 other.

Query Match 74.4%, Score 1566, DB 22; Length 1931;
 Best local Similarity 99.7%; Pred. No. 0;
 Matches 1666; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 58 atcaactctggttcggaagaagacgggtgggtgaggaatccgaggaatggagccctc 117
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 QY 118 gtaacctaaggtttggaagacgaagaggtctgtgaggaactgagctgaggggagatc 177
 DB 72 gtaacctaaggtttggaagacgaagaggtctgtgaggaactgagctgaggggagatc 131
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 QY 1895 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 1954
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 QY 1955 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 1979
 DB 1921 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 1945

RESULT 8
 AAK92259
 ID AAK92259 standard; cDNA; 740 BP.
 XX
 AC AAK92259;
 XX
 DT 06-NOV-2001 (first entry)

XX
 DE Human cDNA 5' end sequence. SEQ ID NO: 719.
 XX
 KW Human, full length cDNA, cDNA synthesis, oligo, mapping, ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1140094-A2.
 XX
 PD 05 SEP-2001.
 XX
 PU 07 JUL 2002, 2000EP-0114089
 XX
 PR 08 JUN-1999, 543P-0194486
 PR 11 JAN 2000, 2000JP-018774.
 PR 02 MAY 2000, 2000JP-0183765.
 XX
 PA (HEB-1) HELIX RES INST.
 XX
 PI Ma L, Nishikawa T, Inada T, Hayashi K, Inaki S, Furai Y,
 PI Wakumoto A, Saito T, Saito K, Kikuchi S, Ueki T, Koda H
 XX
 DR WPI; 2001 524255/58.
 XX
 PI 840 Primers useful for synthesizing full length cDNA clones and their
 PI use in genetic manipulation.
 XX
 PS Claim 2, SEQ ID No 719, 1080pp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones, 840 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5' and 3' ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful in clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is the nucleotide
 CC sequence of the 5' end of a cDNA provided in the invention.
 CC Note: the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD ROM format directly from EPO.
 XX
 SQ Sequence 740 BP: 179 A; 193 C; 200 G; 164 T; 4 other;

Query Match: 21.4%; Score 468; DB 22; Length 740;
 Best Local Similarity: 59.6%; Prod. No. 2,607,74;
 Matches: 568; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

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 QY 105 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 164
 DB 61 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 120
 QY 165 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 224
 DB 121 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 180
 QY 225 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 284
 DB 181 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 240
 QY 285 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 344
 DB 241 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 300
 QY 345 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 404
 DB 301 ggttttaaaagaaagctggatgggacaaacatcagatgaagaaacacatctctctcaaaa 360

[illegible]

```

RESIDUE 10
AAF21841
ID   AAF21841 standard; DNA; 463 BP.
XX
AC   AAF21841.
XX
DT   27 MAR 2001 (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 228.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   neurotrophic; neuroprotection; and vitally and lethally; hepatotropic;
KW   antidiabetic; antituberculous; antileish; antileish; antileish; antileish;
KW   antileish; antileish; antileish; antileish; antileish; antileish; antileish;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; chronic disease;
KW   multiple sclerosis; rheumatoid arthritis; fibrotic disease;
KW   cardiovascular disease; wound healing; neurological disease; ds
XX
OS   Homo sapiens.
XX
PN   W0200055174 AL
XX
ID   21 SEP 2000
XX
RF   chrMAR 2000; 2000W055174B1.
XX
PR   12 MAR 1999; 99030142470.
XX
PA   HUMANA 4 HUMAN GENOME REF. INC.
XX

```

Pt Rosen CA, Ruben SM;
 XX
 Lk WPI: 2,006,115,15/58;
 Dr P-ESTdb: AAB59938;
 XX
 Pl New human breast and ovarian cancer associated gene sequences and the
 Pl polypeptides encoded by these genes, useful in the prevention,
 Pl treatment and diagnosis of cancer, immune disorders, cardiovascular
 Pl disorders and neurological diseases -
 XX
 PS Claim 1: Page 65; 129pp; English.
 XX
 CC Sequences AAF20114 - AAF20231 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22042 - AAF22049 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention, the breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic, immunosuppressive,
 CC neoprotective, neuroprotective, antiviral, antiallergic, hepatotropic,
 CC antidiabetic, antiinflammatory, anticancer, vulnerary, anticonvulsant,
 CC antibacterial, antifungal, antiparasitic and cardiant activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and antagonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis, cardiovascular disorders such as
 CC myocardial ischaemia; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy, and infectious diseases.
 XX
 SQ Sequence 402 BP: 150 A, 90 C, 89 G, 11 T, 1 other.

Query Match: 16.7%; Score 454; DB 21; Length 101;
 Best Local Similarity: 96.6%; Pred. No. 5,66-129;
 Matches 450; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy 546 aatacatgcaaatggatcatlaaataaactgaactc tcatataggaaaacgaatatacctatga 605
 Db 1 aatacatgcaaatggatcatlaaataaactgaactc tcatataggaaaacgaatatacctatga 60
 Qy 606 ttgcttggccatttgagatttggatcatctgaatgaatttggccttggtatgaatttctgag 655
 Db 60 ttgcttggccatttgagatttggatcatctgaatgaatttggccttggtatgaatttctgag 120
 Qy 656 acaatataactctctcttacttcacatgaatcagaagacacgaatatacttatttgaaga 725
 Db 121 acaatataactctctcttacttcacatgaatcagaagacacgaatatacttatttgaaga 180
 Qy 726 atgattttatatttgaatttgatttttggttttatcaagtatttattatgatttga 795
 Db 181 atgattttatatttgaatttgatttttggttttatcaagtatttattatgatttga 240
 Qy 796 cagatttcaggaatctgaggaatttgacacacagatggaagagacatttatttatatgacattg 845
 Db 241 cagatttcaggaatctgaggaatttgacacacagatggaagagacatttatttatatgacattg 300
 Qy 846 aaactatagaacctgagacaaaatcaagggtcagatatacgaagacgatatatataagctatg 905
 Db 301 aaactatagaacctgagacaaaatcaagggtcagatatacgaagacgatatatataagctatg 360
 Qy 906 caattatcacatggaaattgttatccagaaacagccttttgaagatgtcccaatcctt 965
 Db 361 caattatcacatggaaattgttatccagaaacagccttttgaagatgtcccaatcctt 420
 Qy 966 tgcagataaatgtatataatgtatgcacaaaggacat 997
 Db 421 tgcagataaatgtatataatgtatgcacaaaggacat 452

RESULT 11

AAV33547
 ID AAV33547 standard; cDNA: 210 BP;
 XX
 AC AAV33547;
 XX
 DI 29 Dec 1998 (first entry)
 XX
 DE Clone 156108 cDNA fragment encoding a human protein kinase homolog.
 XX
 KW Protein kinase; cell signalling; inflammation; carcinoma; diabetes;
 KW human X linked agammaglobulinemia; nonspherocytic haemolytic anaemia;
 KW artherosclerosis; glioma; testisosis; cholera based septic shock;
 KW 031064 Dictyostelium Y kinase; ss.
 XX
 OS Homo sapiens.
 XX
 PN US5817479-A.
 XX
 PD 06 Oct 1998.
 XX
 PF 02 AUG 1996; JGUS 0700575
 XX
 PR 02 AUG 1996; JGUS 0700575
 XX
 PA (1997) INVENTION (HARK 1997).
 XX
 PI An Young J, Bandman J, Hawkins PR, Wilde CG;
 XX
 DR WI, 1998 5/660717.
 XX
 Pl human kinase polynucleotide(s) and recombinant products useful
 Pl for identification of modulators of the enzyme, and treatment of
 Pl diseases associated with abnormal kinase expression
 XX
 PS Claim 1: Columns 45-48; 49pp; English.
 XX
 CC This invention provides polynucleotides which encode a novel protein
 CC kinase homologous to the human Y kinase and related kinases. The
 CC present sequence represents the clone 156108 cDNA fragment derived from
 CC a human cDNA library designated 100-1 phorbol LPS. The cDNA encodes a
 CC protein kinase which shows homology to the AAF01064 Dictyostelium Y
 CC kinase. Yeast and host cells can be used for recombinant production
 CC of the protein kinase homolog. The recombinant proteins may be used to
 CC clone antibodies for use as anti-kinase therapeutics. Polynucleotides
 CC based on the polynucleotide sequences, i.e. probes and antisense
 CC constructs, the peptides and antibodies are claimed to be useful as
 CC tools for studying signalling cascades in cells and proteins, and for
 CC identifying inhibitors (drugs) to treat diseases and inflammatory
 CC conditions associated with abnormal kinase expression. Diseases that
 CC are claimed to be treatable include human X linked agammaglobulinemia,
 CC nonspherocytic haemolytic anaemia, artherosclerosis, carcinomas,
 CC diabetes, gliomas, testisosis, cholera based septic shock, etc.
 XX
 SQ Sequence 210 BP: 74 A, 40 C, 41 G, 55 T, 0 other

Query Match: 10.0%; Score 210; DB 19; Length 210;
 Best Local Similarity: 100.0%; Pred. No. 6,126-74;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 844 tgaagacctatatacttgagaaagaaatcaagacacagatatacgaacatataatataagctat 905
 Db 1 tgaagacctatatacttgagaaagaaatcaagacacagatatacgaacatataatataagctat 60
 Qy 904 tgaagacctatatacttgagaaagaaatcaagacacagatatacgaacatataatataagctat 965
 Db 61 tgaagacctatatacttgagaaagaaatcaagacacagatatacgaacatataatataagctat 120
 Qy 964 tgaagacctatatacttgagaaagaaatcaagacacagatatacgaacatataatataagctat 1023
 Db 121 tgaagacctatatacttgagaaagaaatcaagacacagatatacgaacatataatataagctat 180
 Qy 1024 gccatataatatacctcaccgaacagatata 1055

151. $\frac{1}{2} \log_2 A(10^6) = 2000$ (11581 entries)

XX
DE Novel human polynucleotide, SEQ ID NO. 481
AA
KW Human: cytostatic; gene therapy; colon cancer; prostate cancer;
KW breast cancer; lung cancer; cancer detection; ss.
XX
OS Homo sapiens.
XX
PN W0200102558-A2.
XX
ID 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-081837A.
XX
PR 02-JUL-1999; 9908-0142310.
PR 02-JUL-1999; 9908-0142311.
XX
PA (CHIK) CHIKEN CORP.
PA (DYSE-) DYSE- INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
PI Reinhard C, Randazzo F, Kennedy GC, Liu D, Lamson G, Drmanac R;
PI Orkajakovic R, Drmanac S, Drmanac M, Liht I, Lishchitz D;
PI Kila D, Garcia V, Jones LW, Strachan R;
XX
DE WPI: 2001-09190710.
XX
PT Library of polynucleotides for diagnosing a cancerous state of a
PT mammalian cell and detecting cancer, particularly of the colon or
PT prostate, comprises 3351 human polynucleotide sequences -
XX
PS Claim 9; Page 613; 1046pp; English.
XX
CC The present sequence is one of 3351 sequences in a library of human
CC polynucleotides. The library is used to detect differentially expressed
CC genes correlated with a cancerous state of a mammalian cell and can
CC detect colon, prostate, breast and lung cancer. The library can be used
CC to produce probes for detection of mRNA and to produce additional copies
CC of the polynucleotides. The probes can be used for chromosome mapping of
CC the polynucleotide and for detection of transcription levels. Ribozymes
CC or antisense oligonucleotides can be generated. The polynucleotides and
CC their gene products are used as genetic or biochemical markers (e.g. in
CC blood or tissues) that will detect the earliest changes along the
CC carcinogenic pathway and/or predict the efficacy of therapies and
CC preventive interventions. The polynucleotides, polypeptides and
CC antibodies against them can be used in pharmaceutical compositions to
CC treat the cancers and proliferative disorders such as neoplasia,
CC dysplasia and hyperplasia.
XX
SQ Sequence 349 BP; 126 A; 70 C; 58 G; 95 T; 0 others;

Query Match 1.00; Score 98; Mb 22; Length 449;
Best Local Similarity 100.0%; Pred. No. 26 05;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2061 atttttgaiaaiaaiaaiaaiaaiaaiaaiaaiaa 2098
DE 247 atttttgaiaaiaaiaaiaaiaaiaaiaaiaaiaa 284

RESULT 15
AAC79976
ID AAC79976 standard, cDNA; 2082 BP.
XX
AC AAC79976;
XX
DI 12 FEB-2001 (first entry)
XX
DE Human secreted protein encoding cDNA for gene 29.
XX
KW Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective;

KW neotropic; neuroprotective; antibacterial; virucide; tumoricide;
KW ophthalmological; vulvatory; gene therapy; treatment; autoimmune disease;
KW hyperproliferative disorder; cardiovascular disorder; ocular disorder;
KW cerebrovascular disorder; nervous system disorder; infectious skin agent;
KW wound healing; epithelial cell proliferation; transplantation; ss.

XX
OS Homo sapiens.
XX
PN W0200058357-A1.
XX
ID 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-080723.
XX
PR 26-MAR-1999; 9908-0126500.
PR 07-JAN-2000; 200003-0174952.
XX
PA (HUMA) HUMAN GENOME SCI INC.
XX
PI Rosen MA, Rubin EM, Komatsu S;
XX
DE WPI: 2000-611704/50.
DE P-PRI: AAB45053

XX
PI Nucleic acid molecules encoding human secreted proteins, used in
PI preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PI Parkinson's diseases and cancers

XX
PS Claim 1a; Page 356-357; 418pp; English.

XX
CC This invention describes novel isolated nucleic acid molecules (I)
CC encoding a human secreted proteins (II) which have immunosuppressive,
CC antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiac,
CC vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,
CC virucide, tumoricide, ophthalmological and vulvatory activity, and can be
CC used for gene therapy. (I) and (II) are used to prevent, treat or
CC ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. (I) and (II) are also used in
CC diagnosing a pathological condition or susceptibility to a pathological
CC condition. The antibodies to (II) can also be used in alleviating
CC symptoms associated with the disorders and in diagnostic immunoassays
CC e.g. radioimmunoassays or enzyme-linked immunosorbent assays (ELISA).
CC Disorders which are diagnosed or treated include autoimmune diseases
CC e.g. rheumatoid arthritis, hyperthyroidism, disorders e.g. neoplasms
CC of the breast or liver, cardiovascular diseases e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous
CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi and ocular diseases e.g. corneal infection. The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotherapy. The polypeptides can also be
CC used as a food additive or preservative to increase or decrease storage
CC capabilities.

XX
SQ Sequence 2082 BP; 584 A; 440 C; 123 G; 911 T; 0 others;

Query Match 1.00; Score 98; Mb 21; Length 2082;
Best Local Similarity 100.0%; Pred. No. 1,600,05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2061 attttgaiaaiaaiaaiaaiaaiaaiaaiaaiaa 2098
DE 2029 attttgaiaaiaaiaaiaaiaaiaaiaaiaaiaa 2066

Search completed: May 14, 2002, 21:47:01
Job time: 8577 sec


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RESULTS      1
AB2777
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  ZONE      1
  DNA       1
  FILTER    1
  FILE      21 JAN 2010
DEFINITION   Sequence from Patient W085507
AB2777
VERSION      AB2777.1 116732464
KEYWORDS
SOURCE       unidentified
  ORGANISM   unidentified
  UNCLASSIFIED
REFERENCE    1 (bases 1 to 2098)
  AUTHORS   BOLDIN M. and WALLACH D.
  TITLE     HUMANIZED CD4 TRANSGENIC MICE DEVELOPED AS CD4 GRAFT AND CELL
  JOURNAL   SURVIVAL PATHWAYS
  EDITOR    FATHALLAH W. 199507 A 10 DECEMBER 1995
  FEATURES   BOLDIN MARK (1); WALLACH DAVID (1)
  SOURCE    1 (bases 1 to 2098)
  ORGANISM   "unidentified"
  DBLINK    "Genbank:26644"
BASE COUNT   549 a 452 c 449 g 529 t
ORIGIN

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Query Match 81.98, Score 1719; DB 9; Length 1898;

[illegible]

[illegible][illegible]

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Qy 718 atttggacaaatgaatttcatgtttaaagattgagatttgggtttatcaaaagtgccgcatgat 777
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Qy 778 atccctctccagctcaggaagtagcaaatctgcac tagaaggaggggacaattatttatat 837
Db 732 gtccctctccagctcaggaagtagcaaatctgcac tagaaggaggggacaattatttatat 791
Qy 838 gccacctgaaaactatgaacctggacaaaaatcaa gggccagatcgaagcagcatatata 897
Db 742 gccacctgaaaactatgaacctggacaaaaatcaa gggccagatcgaagcagcatatata 851
Qy 898 taatttatgaaatgacatggaattgttatccaaiaaaacagccttttgaagatgtcac 957
Db 852 taatttatgaaatgacatggaattgttatccaaiaaaacagccttttgaagatgtcac 911
Qy 958 caatctctgagagataatgttatagtgatcacaatgacatgacatgttatttaattgaaga 1017
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Db 972 aatgtttgacatgatgataaactcagcagagagagta gactctcttaattagaagaatgagatg 1031
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Qy 1258 gtttgaagagatgttgaagagagatgttctctctaaatgttttattagaatgaaagagat 1317
Db 1212 gtttgaagagatgttgaagagagatgttctctctaaatgttttattagaatgaaagagat 1271
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Qy 1678 atctagaagagagagagagagagagagagagagagagagagagagagagagagagagagag 1737
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Db 1812 tttaacttcaaaataaaagagatgaagtgacgttttttgaagagagagagagagagagagag 1871
Qy 1918 aqqaalattata 1929
Db 1872 aggaattattata 1884

RESULT 4
AF027706 2501 bp mRNA linear PRI 10-SEP-1998
LOCUS Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
DEFINITION
ACCESSION AF027706
VERSION AF027706.1 GI:124886
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2501)
Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis
J. Biol. Chem. 273 (15), 12767-12770 (1998)
98241596
REFERENCE
2 (bases 1 to 2501)
Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G.
Direct Submission
Submitted (01-OCT-1997) Dept. Pathology, Comprehensive Cancer & Geriatrics Center, 4-131 CGGC 1500 P. Medical Center Dr, Ann Arbor, MI 48109, USA
FEATURES
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1..2501
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/chromosome="8"
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/function="regulates apoptosis"
/notes="CARD domain protein; phosphorylated protein; phosphorylated protein, apoptosis regulator"
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2479..2484
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/gene="RICK"
BASE COUNT 768 a 535 c 459 g 699 t
ORIGIN

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RESULTS	5
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LOCUS	AF064824 1502 bp. mRNA. Features: 181 bp ORF. Pro
DEFINITION	Homo sapiens CARK-related amino-acyl-tRNA-associated kinase mRNA, clone
ACCESSION	AF064824
VERSION	AF064824.1 (21 JUL 1997)

[illegible]

Df	405	CTGCTCGACAGTGAAGAAAGAGATGCTCTAAGAGAAGCTGAAATTTACACAAAGCTACA	464
Qy	482	TTTAACTTACATTTTCCAAATTTTGGGAATTTGCAATGAGGCTGAATTTTGGGAATAGTT	541
Df	465	TTTATTACATTTTCCAAATTTTGGGAATTTGCAATGAGGCTGAATTTTGGGAATAGTT	524
Qy	542	TTTAACTTACATTTTCCAAATTTTGGGAATTTGCAATGAGGCTGAATTTTGGGAATAGTT	601
Df	525	ACTGAATACATGTCAAATGATCATTAATGAACTGCTACATAGGAAGACGAAATATCTT	584
Qy	602	GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	661
Df	585	GATGTTGCTTGGCATTTGATGATTTGCAATGCTGTCATGAAATTTGGCTTTGGTGAATTTAC	644
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Df	645	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	704
Qy	722	GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	781
Df	705	GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	764
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Df	765	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	824
Qy	842	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	901
Df	825	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	884
Qy	902	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	961
Df	885	TATGTCAGTTATCATATGGAAGATGTTATTCAGAAAAACAGCTTTTGAAGATGTCACCAAT	944
Qy	962	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	1021
Df	945	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	1004
Qy	1022	TTTCAAAATTAAGCTGCTGCTTACCTTCACTCACTCACTCACTCACTCACTCACTCACT	1081
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Shewchuk, V., Weeber, G. D., & Beckstein, S. (2001). *Standardized S.M.C.*

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RI J. Biol. Chem. 273:16299-16309(1998).
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RX MEDLINE 98167936; PubMed 9512209;
RA Mennelly J.W., Hsu J., Bury M.;
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RI Kinase."
RI J. Biol. Chem. 273:16081-16075(1998)
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RA Thum B., Holman K., Pann K., Martinon F., Bodmer J.-L.;
RA Mennelly J., Kischkel J.;
PI "Identification of cIAP1 (R100) as a R100-like kinase that associates with
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RI Curr. Biol. 8:100(1998)

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RECORD 15
018645
ID 018645 PRELIMINARY PRI: 582 AA
AC 018645; Q9U4G0;
DT 01 JAN 1998 (TrEMBLrel. 05, Created)
DT 01 JAN 1998 (TrEMBLrel. 05, Last sequence update)
DT 01 DEC 2001 (TrEMBLrel. 19, Last annotation update)
GI SWIAA_PRTA12IN (SWIAA_PRTA12IN).
GN SWIAA OR IG_1228.2 OR CG4051.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota, Metazoa, Arthropoda, Insecta, Hexapoda, Insecta,
OC Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
OC Tephritidae, Tephritidae, Drosophila.
OX NCBI_taxonomy:7327;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN DESIGNATION:
RX KIRKLAND 20196900; PubMed 10741112;
RA Adams M.L., Schilke J.L., Holt R.A., Lewis C.A., Seaynne J.D.,
RA Anagnostou P.G., Scherer S.E., Li P.W., Hoskins P.A., Gallo R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell B.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.P., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.J., Holt R.A., Nelson C.E., Miklos G.L.D.,
RA Abril J.F., Adayaraj A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballow R.M., Basu A., Bjornvad L., Bayraktarov I., Beasley E.M.,
RA Benson R.Y., Besos F.V., Betman K., Bhattacharya S.,
RA Borokov D., Botkin M.B., Bozinger K., Brickstein M., Brottier P.,
RA Burks K.C., Busan D.A., Butler J., Cadieu E., Center A., Chandra I.,
RA Cherry J.H., Chesley S., Dulake G., Faenert J., Davies P.,
RA de Pablo R., Deitcher A., Deng Z., Mays A.D., Dowling J., Dietz S.M.,
RA DeRubeis E., Dong L.E., Downes M., Duran-Rocha S., Funk D.J., Dunn P.,
RA Durbin R.J., Evangelista C.C., Fortez C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellan A.E., Garq N.S., Gelbart W.M., Glasser K.,
RA Glusker A., Gong F., Gorrell T.H., Gu Z., Guan X., Harris M.,
RA Hartzel N.I., Hickey D., Horn G.T., Hernandez J., Horak J.,
RA Hummer D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jacobi H., Jacobson F., Karpius L.B., Ke Y., Kennedy J.A., Ketchum V.A.,
RA Kimmel B.E., Kodira C.B., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Lechsky A.A., Li J., Li Z., Liang Y., Liu X.,
RA Liu X., Mattei P., McIntosh J.C., McLeod M.P., Melphetson D.,
RA Mickelson G., Millick D.V., Miriam C., Mori S., Montefiore A.,
RA Mount S.H., Moy B., Murphy B., Murphy L., Murry L.M., Nelson D.L.,
RA Olsin D.F., Olson E.A., Olson K., Osterberg K.K., Palczewski J.M.,
RA Patrzyk M., Pittman G.S., Pan S., Pollard J., Port V., Reese M.G.,
RA Reibert P., Remington K., Saunders R.D.C., Schoeler E., Shen H.,
RA Shon R.C., Siden-Kimons I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stroba K., Sun E.,
RA Svirskaas K., Taylor C., Turner K., Venter E., Wang A.B., Wang X.,
RA Wang Z. Y., Wasserman D.A., Weststock G.M., Weissbach J.,
RA Williams S.M., Woodruff I., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yin F., Yin L., Yin S., Yin M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhu J.H., Zhou W., Zhou X., Zhu J., Zhu X., Smith B.O.,
RA Zuker C.A., Zuker S.W., Zuker J.M., Venter D.J.;
RT "The genome sequence of Drosophila melanogaster."
RI Science 287(5414), 215-216(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN DESIGNATION:
RA Taborda E.N., Hickey D.A.;
E Submitted (Aug 2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN DESIGNATION:
RA Taborda E.N., Hickey D.A.;
E Submitted (Oct 2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN DESIGNATION:
RA Papapanakis S., Spanos I., Cox S., Siden Kimons I., Louis C.;
E Submitted (Jul 2000) to the EMBL/Genbank/DBJ databases.

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01 01-DEC-2001 (TrEMBLrel. 19, Created)
 02 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 03 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 04 NIMA-RELATED KINASE B.
 05 NEK8.
 06 Brachycephalus pinnatus (Zebrafish) (Shihai Jiao).
 07 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 08 Actinopterygii; Neopterygii; Characii; Euteleostei; Ostariophysi;
 09 Cypriniformes; Cyprinidae; Danio
 10 NIMA_taxonomy=7655;
 11
 12 SEQUENCE FROM N.A.
 13 Liu S., Lu W., Obara-Ishihara T., Drummond L., Beier D.R.;
 14 "A defect in a novel Nek-family kinase causes cystic disease in the
 15 mouse and in zebrafish."
 16 Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases
 17 EMBL: AF407589; AAF98675.1;
 18 Kinase.
 19 SEQUENCE 697 AA; 76541 MW; 875A51D1E3831AA7 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 697;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 146 DEKFNILLD 155
 111111111
 DB 128 DEKFNILLD 137

RESULT 8
 Q91ZR4
 ID Q91ZR4 PRELIMINARY; PRI: 698 AA.
 AC Q91ZR4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 02 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 03 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 04 NIMA-RELATED KINASE B.
 05 NEK8.
 06 Mus musculus (Mouse).
 07 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 08 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 09 NIMA_taxonomy=10099;
 10
 11 SEQUENCE FROM N.A.
 12 STRAIN:297BL/6J;
 13 Liu S., Lu W., Obara-Ishihara T., Drummond L., Beier D.R.;
 14 "A defect in a novel Nek-family kinase causes cystic disease in the
 15 mouse and in zebrafish."
 16 Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 17 EMBL: AF407579; AAF98675.1;
 18 Kinase.
 19 SEQUENCE 698 AA; 75264 MW; 680B29A87188E94 CRC64;

Query Match 1.9%; Score 10; DB 1; Length 698;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 146 DEKFNILLD 155
 111111111
 DB 128 DEKFNILLD 137

RESULT 9
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 ID Q9GJ85 PRELIMINARY; PRI: 22 AA.
 AC Q9GJ85;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 02 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 03 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 04 CA2+INDEPENDENT IN-DEPENDENT KINASE (FRAGMENT).
 05 Lagenorhynchus obliquidens (Pacific white-sided dolphin).

06 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 07 Mammalia; Eutheria; Cetartiodactyla; Cetacea; Monodelphi; Delphinidae;
 08 Lagenorhynchus.
 09 NIMA_taxonomy=90247;
 10
 11 SEQUENCE FROM N.A.
 12 STRAIN:VARS142RW; MW: 2.1 kDa;
 13 Bare M.P., Cipriano P., Palermo S.R.;
 14 "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
 15 Speciation, Systematics and Conservation."
 16 Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 17 EMBL: AF140810; AAF98663.1;
 18 EMBL: AF140809; AAF98662.1;
 19 Kinase.
 20 NON-IBK 1 1
 21 NON-IBK 2 2
 22 SEQUENCE 22 AA; 2349 MW; AAF16A00N-AF140809 CRC64;

Query Match 1.7%; Score 9; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 161 KIADFGILSK 169
 111111111
 DB 8 KIADFGILSK 16

RESULT 10
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 ID Q9GJ80 PRELIMINARY; PRI: 33 AA.
 AC Q9GJ80;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 02 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 03 01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
 04 CA2+INDEPENDENT IN-DEPENDENT KINASE (FRAGMENT).
 05 Lagenorhynchus obliquidens (Pacific white-sided dolphin).
 06 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 07 Mammalia; Eutheria; Cetartiodactyla; Cetacea; Monodelphi; Delphinidae;
 08 Lagenorhynchus.
 09 NIMA_taxonomy=27011;
 10
 11 SEQUENCE FROM N.A.
 12 STRAIN-VARIABLES STRAINS;
 13 Bare M.P., Cipriano P., Palermo S.R.;
 14 "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
 15 Speciation, Systematics and Conservation."
 16 Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 17 EMBL: AF140820; AAF98676.1;
 18 EMBL: AF140813; AAF98666.1;
 19 EMBL: AF140814; AAF98667.1;
 20 EMBL: AF140817; AAF98670.1;
 21 EMBL: AF140818; AAF98671.1;
 22 EMBL: AF140819; AAF98672.1;
 23 InterPro: IPR000719; Euk. pkinase
 24 Pfam: PF00069; pkinase; 1.
 25 PROSITE: PS50044; PROSITE_KINASE_DOM; 1.
 26 All binding, Kinase; TransDomain.
 27 NON-IBK 1 1
 28 NON-IBK 2 2
 29 SEQUENCE 33 AA; 3564 MW; 064A909F390001 CRC64;

Query Match 1.7%; Score 9; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 161 KIADFGILSK 169
 111111111
 DB 8 KIADFGILSK 16

RESULT 11

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> Q96JV7
> Q96JV7;
> 01-MAR-2001 (TrEMBLrel. 16, Created)
> 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
> 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
> CAZ / GAGGAGGGIN / GAGGAGGGIN KINASE (FRAGMENT);
> Lagenorhynchus obliquidens (Pacetic white-sided dolphin);
> Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;
> Mammalia; Eutheria; Cetartiodactyla; Cetacea; suborder; Delphinida;
> Lagenorhynchina;
> NCBI TaxID: 9612;
> [1]
> SEQUENCE FROM N.A.
> STRAIN: J05_236_10, AND J05_246;
> Hsu M.P., Cipriani P., Palmi S.R.;
> "New Evaluation of Genetic Monophyly in Delphinus: Implications for
> Speciation, Systematics and Conservation.";
> Submittal (APR 1999) to the EMBL/GenBank/DBJ databases;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> Enzyme: PR000719; Pnk_pkinase
> Enzyme: PF00069; pkinase 1;
> PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
> A/P binding; Kinase; Transferase;
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> NON_TER 34 43
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Query Match 1.78; Score 9; DB 6; Length 33;
Best Local Similarity 100.0%; Prod. No. 014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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> 01-MAR-2001 (TrEMBLrel. 16, Created)
> 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
> 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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> Lagenorhynchus obliquidens (Pacetic white-sided dolphin);
> Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;
> Mammalia; Eutheria; Cetartiodactyla; Cetacea; suborder; Delphinida;
> Lagenorhynchina;
> NCBI TaxID: 9612;
> [1]
> SEQUENCE FROM N.A.
> STRAIN: J05_236_10, AND J05_246;
> Hsu M.P., Cipriani P., Palmi S.R.;
> "New Evaluation of Genetic Monophyly in Delphinus: Implications for
> Speciation, Systematics and Conservation.";
> Submittal (APR 1999) to the EMBL/GenBank/DBJ databases;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> Enzyme: PR000719; Pnk_pkinase
> Enzyme: PF00069; pkinase 1;
> PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
> A/P binding; Kinase; Transferase;
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> 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
> 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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> Lagenorhynchus obliquidens (Pacetic white-sided dolphin);
> Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;
> Mammalia; Eutheria; Cetartiodactyla; Cetacea; suborder; Delphinida;
> Lagenorhynchina;
> NCBI TaxID: 9612;
> [1]
> SEQUENCE FROM N.A.
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> Hsu M.P., Cipriani P., Palmi S.R.;
> "New Evaluation of Genetic Monophyly in Delphinus: Implications for
> Speciation, Systematics and Conservation.";
> Submittal (APR 1999) to the EMBL/GenBank/DBJ databases;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> Enzyme: PR000719; Pnk_pkinase
> Enzyme: PF00069; pkinase 1;
> PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
> A/P binding; Kinase; Transferase;
> NON_TER 1 1
> NON_TER 34 43
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Query Match 1.78; Score 9; DB 6; Length 33;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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> 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
> 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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> Lagenorhynchus obliquidens (Pacetic white-sided dolphin);
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> Mammalia; Eutheria; Cetartiodactyla; Cetacea; suborder; Delphinida;
> Lagenorhynchina;
> NCBI TaxID: 9612;
> [1]
> SEQUENCE FROM N.A.
> STRAIN: J05_236_10, AND J05_246;
> Hsu M.P., Cipriani P., Palmi S.R.;
> "New Evaluation of Genetic Monophyly in Delphinus: Implications for
> Speciation, Systematics and Conservation.";
> Submittal (APR 1999) to the EMBL/GenBank/DBJ databases;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
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> Enzyme: PR000719; Pnk_pkinase
> Enzyme: PF00069; pkinase 1;
> PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
> A/P binding; Kinase; Transferase;
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> NON_TER 34 43
> SEQUENCE 34 AA: 6508 MW: 6611FD1CA750DE01 CRC64;

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> 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
> 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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> Mammalia; Eutheria; Cetartiodactyla; Cetacea; suborder; Delphinida;
> Lagenorhynchina;
> NCBI TaxID: 9612;
> [1]
> SEQUENCE FROM N.A.
> STRAIN: J05_236_10, AND J05_246;
> Hsu M.P., Cipriani P., Palmi S.R.;
> "New Evaluation of Genetic Monophyly in Delphinus: Implications for
> Speciation, Systematics and Conservation.";
> Submittal (APR 1999) to the EMBL/GenBank/DBJ databases;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> Enzyme: PR000719; Pnk_pkinase
> Enzyme: PF00069; pkinase 1;
> PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
> A/P binding; Kinase; Transferase;
> NON_TER 1 1
> NON_TER 34 43
> SEQUENCE 34 AA: 6508 MW: 6611FD1CA750DE01 CRC64;

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Query Match 1.78; Score 9; DB 6; Length 33;
Best Local Similarity 100.0%; Prod. No. 014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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> Q96JV7;
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> 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
> 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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> Lagenorhynchus obliquidens (Pacetic white-sided dolphin);
> Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;
> Mammalia; Eutheria; Cetartiodactyla; Cetacea; suborder; Delphinida;
> Lagenorhynchina;
> NCBI TaxID: 9612;
> [1]
> SEQUENCE FROM N.A.
> STRAIN: J05_236_10, AND J05_246;
> Hsu M.P., Cipriani P., Palmi S.R.;
> "New Evaluation of Genetic Monophyly in Delphinus: Implications for
> Speciation, Systematics and Conservation.";
> Submittal (APR 1999) to the EMBL/GenBank/DBJ databases;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> EMBL: AF140815; AAF98666.1;
> Enzyme: PR000719; Pnk_pkinase
> Enzyme: PF00069; pkinase 1;
> PROSITE: PS0011; PROTEIN_KINASE_DOM; 1;
> A/P binding; Kinase; Transferase;
> NON_TER 1 1
> NON_TER 34 43
> SEQUENCE 34 AA: 6508 MW: 6611FD1CA750DE01 CRC64;

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F1 NON_TER 33 33
 SQ SEQUENCE 33 AA: 5604 MW: 6604AY09F3510EQ1 CR064;

Query Match 1.7%; Score 9; L3 6; Length 33;
 Best Local Similarity 100.0%; Prod. No. 3.14;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KIA060L5K 169
 DB 16 KIA060L5K 27

KRR001 15
 Q38987
 ID Q38987 PRELIMINARY; PRI: 55 AA.
 AC Q38987;
 DI 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
 DI 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE PROTEIN KINASE CATALYTIC DOMAIN (FRAGMENT).
 GN AKZ1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OX Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OX eucosids 11; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_taxid 3702;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN RH. 0; TISSUE LEAF;
 KX MEDLINE 96124233; PubMed 8534852;
 KA Thummler F., Kirchner M., Tenber K., Dietrich P.;
 PI "Differential accumulation of the transcripts of 22 novel protein
 KE kinase genes in Arabidopsis thaliana.";
 KL Plant Mol. Biol. 29:561-565(1995).
 DR EMBL: X86966; CAA60529.1; -;
 DR InterPro: IPR000719; Euk_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 55 AA: 5910 MW: 9E55D60BD25 A9FB CR064;

Query Match 1.7%; Score 9; L3 10; Length 55;
 Best Local Similarity 100.0%; Prod. No. 3.2;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 VKIA06GLS 168
 DB 13 VKIA06GLS 21

Search completed: May 13, 2002, 21:37:13
 Job time: 366 sec



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A2AR / A2ARP STANDARD: PRI: 448 AA.
AC Q66475;
DT 01 NOV 1997 (Rel. 35, Created)
DI 01 NOV 1997 (Rel. 35, Last sequence update)
DI 16 OCT 2001 (Rel. 40, Last annotation update)
DE Alpha 2B adrenergic receptor (Alpha-2B adrenoceptor).
GN A2AR.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricomorpha; Caviidae; Cavia.
OX NCBI TaxID: 10141;
RN 111
RP SEQUENCE FROM NIA.
RC STIPAIN HARTLEY;
RX REFLINE 9615257; PubMed 8573196;
RA Svensson S.P., Bailey L.D., Porter A.C., Ricman J.G., Regan J.W.;
PT "Heterologous expression of the cloned guinea pig alpha 2A, alpha 2B,
RI and alpha 2C adrenoceptor subtypes. Radioligand binding and
RT functional coupling to a GAMP-responsive reporter gene.";
RI Biochem. Pharmacol. 51:291-303(1995).
CC -1 FUNCTION: ALPHA 2 ADRENERGIC RECEPTOR RELEVANT FOR CATECHOLAMINE-
CC RECEPTOR INHIBITION OF ADENYLATE CYCLASE FOR GPCR PROTEINS.
CC
CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS.
CC
CC .....
CC This SWISS Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
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CC entities is prohibited. For more information, please contact the EBI
CC or send an email to licenstat@ebi.ac.uk.
CC .....
DR EMBL: U25724; AAA07075.1;
DR InterPro: IPR012275; GPCR_Rhodopsn.
DR Pfam: PF00001.7; 1;
DR PROSITE: PROSITE_1; GPCR_PROSITE.
DR PROSITE: PROSITE_2; GPCR_PROSITE_2; 1;
KW G protein-coupled receptor; Transmembrane; Multitene Family;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 12 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 13 38 1 (POTENTIAL).
FT DOMAIN 39 49 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 50 75 2 (POTENTIAL).
FT DOMAIN 76 95 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 96 108 3 (POTENTIAL).
FT DOMAIN 109 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 171 4 (POTENTIAL).
FT DOMAIN 172 188 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 189 192 5 (POTENTIAL).
FT DOMAIN 193 205 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 206 231 6 (POTENTIAL).

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RESULTS      1
K0174 HUMAN
ID K0174 HUMAN          GI440430,      1st;      373 AA
AC Q16560;
DT 01-NOV-1997 (Ref. 15, Created)
PI 01-NOV-1997 (Ref. 15, Last sequence update)
UI 16-Jul-2000 (Ref. 40, Last annotation update)
DE Calcium/calmodulin dependent protein kinase type IV catalytic chain
DE (pI 2.7-3.1; 37AM kinase-33) (p50ME IV) (p100meas; Calsperrin)
GN pAKK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Mammalia; Euteleostomi;
OC Mammalia; Eulipotyria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID: 9606;
RN [1]
RP SEQUENSE FROM N.A.
RX REF ID: 9437404, PubMed 8089075;
RA Kilian L., Okuno S., Fujisawa H.;
RT "cDNA cloning and expression of human calmodulin dependent protein
KI kinase IV. ";
RI 1, Biochem. 115:637-640(1994).
RN [2]
RP SEQUENSE FROM N.A.
RT TISSUE: Cerebellum, and Thymus;
RX REF ID: 9425256, PubMed 8194751;
RA Blaud M.M., Mammie R.S., Ohnsted C.A.;
RT "The cDNA sequence and characterization of the

```

RI Ca2+/calmodulin-dependent protein kinase α from human brain and
 RI thymus.",
 RI Gene 142:191-197(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RF TISSUE: Brain;
 RX MEDLINE 9111962; PubMed 8107110;
 RA Moskalov G., Hanissian S.D., Jawahar S., Vora L., Kiehl K.,
 RA Chaitlin L.A.;
 RI "A Ca2+/calmodulin-dependent protein kinase C α kinase is expressed
 RI after transformation of primary human Polyphocytes by Epstein Barr
 RI virus (EBV) is induced by the EBV oncogene LMP1";
 RI J. Virol. 68:1697-1705(1994).
 CC -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
 CC PROTEIN.
 CC -!- CATALYTIC ACTIVITY: ATP + protein -> ADP + O-phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
 CC NUCLEI (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
 CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
 CC SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC or send an email to license@ebi-sib.ch).
 CC -----
 DR EMBL: D33742; BAA06463.1; -;
 DR EMBL: F12900; AAA5539.1; -;
 DR EMBL: L21859; AAA18251.1; -;
 DR DSSP: Q64450; 1A06;
 DR PIR: I14080; -;
 DR InterPro: IPR000719; Euk_pkinase;
 RF InterPro: IPR000719; Ser/Thr_kinase;
 RF Pfam: PF00069; pkinase; 1;
 DR SMART: SM00229; pkinase; 1;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
 DR PROSITE: PS00108; PROTEIN_KINASE_SI; 1;
 DR PROSITE: PS5001; PROTEIN_KINASE_TYR; 1;
 RF TrnSeq: Serine, Threonine, Tyrosine Kinase, At. binding,
 RW Calmodulin-binding; Alternative splicing;
 FT CHAIN 310 473 CALSPERMIN.
 FT DOMAIN 45 300 PROTEIN KINASE
 FT NP_BIND 52 60 ATP (BY SIMILARITY).
 FT BINDING 75 75 ATP (BY SIMILARITY).
 FT ACT_SITE 64 164 HY SIMILARITY.
 FT DOMAIN 322 341 CALMODULIN BINDING (OPTIONAL).
 SQ SEQUENCE 473 AA; 51925 MW; RFFPSIES6 2426DC CRG64;

Query Match 1.7%; Score 9; D:1; Length 475;
 Best Local Similarity 100.0%; Pred. No. 147;
 Matches 9; Mismatches 0; Indels 0; Gaps 0

QY 111 KIAA0GLSK 169
 11111111
 DQ 182 KIAA0GLSK 169

RELEASE 4
 KOC4_RAI
 ID KOC4_RAI STANDARD; PRI: 474 AA.
 AC P13234;
 DI 01-JAN-1990 (Rel. 13, Created)
 DI 01-APR-1993 (Rel. 25, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ca2+/calmodulin-dependent protein kinase type IV catalytic chain
 DE (EC 2.7.1.12) (CAM kinase α) (CAMK IV, α -calmodulin-calpersmin)

RN CAMK1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI TaxID=10116;
 RN [1]
 RI SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE 9128354B; PubMed 1648210;
 RA Olmstedo C.A., Dand M.M., Morfitt B.M., Salyoun N.;
 RI "Calcium/calmodulin-dependent protein kinase and a male germ
 RI cell-specific calmodulin-binding protein are derived from the same
 RI gene";
 RI Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991)
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 9130408; PubMed 1648385;
 RA Means A.R., Trizaloni P., Lamapresse R., Needleman P.S.,
 RA Shachter G.R., and L.;
 RI "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
 RI cell-specific calmodulin-binding protein are derived from the same
 RI gene";
 RI Mol. Cell. Biol. 11:3960-3971(1991).
 RN [3]
 RP SEQUENCE OF 250-474 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE: Brain;
 RX MEDLINE 93174717; PubMed 2548433;
 RA Olmstedo C.A., Jensen K.F., Salyoun N.;
 RI "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
 RI granule cells. Identification of a novel neuronal
 RI calmodulin-dependent protein kinase";
 RI J. Biol. Chem. 264:2081-2087(1989).
 RN [4]
 RP SEQUENCE OF 308-474 FROM N.A., AND SEQUENCE OF 335-361.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE 9312372; PubMed 2914999;
 RA Ong J., Shachter G.R., Cook R.G., Means A.R.;
 RI "Molecular cloning sequence and distribution of rat calpersmin, a
 RI high affinity calmodulin-binding protein";
 RI J. Biol. Chem. 264:2081-2087(1989).
 CC 1. FUNCTION: CALSPERMIN IS A HEAT STABLE, ACIDIC, CALMODULIN BINDING
 CC PROTEIN.
 CC -!- CATALYTIC ACTIVITY: ATP + protein -> ADP + O-phosphoprotein.
 CC -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
 CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
 CC SPLICING.
 CC -!- TISSUE SPECIFICITY: CALSPERMIN IS PREDOMINANTLY FOUND IN MAMMALIAN
 CC TESTIS AND BRAIN.
 CC -!- PFM: THE N-TERMINAL OF CALSPERMIN IS PHOSPHO
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M63344; AAA4685.1; -;
 DR EMBL: M64488; AAA40845.1; ALT_SEQ;
 DR EMBL: M64757; AAA40846.1;
 DR EMBL: M64757; AAA40847.1; -;
 DR EMBL: J04600; AAA11867.1; -;
 DR EMBL: J04446; AAA40850.1; -;
 DR PIR: A11103; TVRPO4;
 DR DSSP: P00518; 1PHK;
 DR InterPro: IPR000719; Euk_pkinase;
 DR InterPro: IPR002233; Ser/Thr_pkinase;
 DR Pfam: PF00069; pkinase; 1;
 DR SMART: SM00229; pkinase; 1;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand
 13 MAIN 300 474 CALDERMIN
 14 DMAIN 19 296 PROTEIN_KINASE
 15 NE_BIND 48 56 ATP (BY SIMILARITY);
 16 BINDING 71 71 ATP (BY SIMILARITY);
 17 ACT_SITE 142 142 BY SIMILARITY;
 18 DETA_R 438 437 CALDERMIN KINETIC (POTENTIAL);
 19 DETA_R 438 437 PLY_RUB
 20 DMAIN 438 438 PLY_RUB
 21 UNRESID 37 422 1 M (IN REF. 2 AND 4)
 22 SEQUENCE 474 AA; 5313 HW; 56071A:564102:22:01064.

Query Match 1 7%; Score 9; DR 1; Length 474;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 0; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand

13 MAIN 300 474 CALDERMIN
 14 DMAIN 19 296 PROTEIN_KINASE
 15 NE_BIND 48 56 ATP (BY SIMILARITY);
 16 BINDING 71 71 ATP (BY SIMILARITY);
 17 ACT_SITE 142 142 BY SIMILARITY;
 18 DETA_R 438 437 CALDERMIN KINETIC (POTENTIAL);
 19 DETA_R 438 437 PLY_RUB
 20 DMAIN 438 438 PLY_RUB
 21 UNRESID 37 422 1 M (IN REF. 2 AND 4)
 22 SEQUENCE 474 AA; 5313 HW; 56071A:564102:22:01064.

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand

13 MAIN 300 474 CALDERMIN
 14 DMAIN 19 296 PROTEIN_KINASE
 15 NE_BIND 48 56 ATP (BY SIMILARITY);
 16 BINDING 71 71 ATP (BY SIMILARITY);
 17 ACT_SITE 142 142 BY SIMILARITY;
 18 DETA_R 438 437 CALDERMIN KINETIC (POTENTIAL);
 19 DETA_R 438 437 PLY_RUB
 20 DMAIN 438 438 PLY_RUB
 21 UNRESID 37 422 1 M (IN REF. 2 AND 4)
 22 SEQUENCE 474 AA; 5313 HW; 56071A:564102:22:01064.

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand

13 MAIN 300 474 CALDERMIN
 14 DMAIN 19 296 PROTEIN_KINASE
 15 NE_BIND 48 56 ATP (BY SIMILARITY);
 16 BINDING 71 71 ATP (BY SIMILARITY);
 17 ACT_SITE 142 142 BY SIMILARITY;
 18 DETA_R 438 437 CALDERMIN KINETIC (POTENTIAL);
 19 DETA_R 438 437 PLY_RUB
 20 DMAIN 438 438 PLY_RUB
 21 UNRESID 37 422 1 M (IN REF. 2 AND 4)
 22 SEQUENCE 474 AA; 5313 HW; 56071A:564102:22:01064.

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand

13 MAIN 300 474 CALDERMIN
 14 DMAIN 19 296 PROTEIN_KINASE
 15 NE_BIND 48 56 ATP (BY SIMILARITY);
 16 BINDING 71 71 ATP (BY SIMILARITY);
 17 ACT_SITE 142 142 BY SIMILARITY;
 18 DETA_R 438 437 CALDERMIN KINETIC (POTENTIAL);
 19 DETA_R 438 437 PLY_RUB
 20 DMAIN 438 438 PLY_RUB
 21 UNRESID 37 422 1 M (IN REF. 2 AND 4)
 22 SEQUENCE 474 AA; 5313 HW; 56071A:564102:22:01064.

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand

13 MAIN 300 474 CALDERMIN
 14 DMAIN 19 296 PROTEIN_KINASE
 15 NE_BIND 48 56 ATP (BY SIMILARITY);
 16 BINDING 71 71 ATP (BY SIMILARITY);
 17 ACT_SITE 142 142 BY SIMILARITY;
 18 DETA_R 438 437 CALDERMIN KINETIC (POTENTIAL);
 19 DETA_R 438 437 PLY_RUB
 20 DMAIN 438 438 PLY_RUB
 21 UNRESID 37 422 1 M (IN REF. 2 AND 4)
 22 SEQUENCE 474 AA; 5313 HW; 56071A:564102:22:01064.

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand

13 MAIN 300 474 CALDERMIN
 14 DMAIN 19 296 PROTEIN_KINASE
 15 NE_BIND 48 56 ATP (BY SIMILARITY);
 16 BINDING 71 71 ATP (BY SIMILARITY);
 17 ACT_SITE 142 142 BY SIMILARITY;
 18 DETA_R 438 437 CALDERMIN KINETIC (POTENTIAL);
 19 DETA_R 438 437 PLY_RUB
 20 DMAIN 438 438 PLY_RUB
 21 UNRESID 37 422 1 M (IN REF. 2 AND 4)
 22 SEQUENCE 474 AA; 5313 HW; 56071A:564102:22:01064.

Query Match 1 7%; Score 9; DR 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

10 PROSITE: PS00109; PROTEIN_KINASE_DOM. 1
 11 TRANSFERASE; Serine/threonine-protein kinase; ATP binding;
 12 Transmembrane domain; 1 strand; Alpha-helices; 1 strand

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RESULT 6
SNF1_SCHPO
ID   SNF1_SCHPO          STANDARD;          PRT:  576 AA.
AC   Q74546;
DT   15-JUN-1999 (Rel. 38, Created)
DI   15-JUN-1999 (Rel. 38, Last sequence update)
DI   15-JUN-1999 (Rel. 38, Last annotation update)
DE   SNF1 like protein kinase (EC 2.7.1. ).
GN   SPOC74.040;
OS   Schizosaccharomyces pombe (Hansen yeast).
OC   Eukaryota; Eukaryota; Ascomycota; Schizosaccharomycetes.
OC   Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomycetes; Candida.
OC   Schizosaccharomycetes.
OX   NCBI_TaxID: 48966;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN: 972;
PA   Murphy, L., Harris, D., Lyne, M., Rajandream, M.A., Barrell, B.G.,
RE   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   SNF1 SUBFAMILY.
CC   -----
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CC   entities requires a license agreement (for http://www.ebi.ac.uk/ebis/ebis/
CC   or send an email to license@ebi.ac.uk).
CC   -----
DR   EMBL: AL041543; CAA20822.1;
DR   HSSP: P03518; 1PHK;
DR   InterPro: IPR000719; Euk_pkinase;
DR   InterPro: IPR002290; Ser_thr_pkinase;
DR   InterPro: IPR004419; MKA;
DR   Pfam: PF00069; pkinase_1;
DR   SMART: SM00220; S_TKc; 1;
DR   PROSITE: PS00167; PROTEIN_KINASE_ATP_1;
DR   PROSITE: PS00168; PROTEIN_KINASE_ST_1;
DR   PROSITE: PS00111; PROTEIN_KINASE_DOM_1;
KW   Transferase; Serine/threonine protein kinase; ATP-binding.
FT   DOMAIN      34   285   PROTEIN KINASE.
FT   NP_BIND     40   48    ATP (BY SIMILARITY).
FT   BINDING     63   63    ATP (BY SIMILARITY).
FT   ACT_SITE    156   156   BY SIMILARITY.
SQ   SEQUENCE  576 AA;  65996 MW;  F5857F8F11F7B50 CRR64;

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Query Match 1.7%; Score 9; DI 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 1.45;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 160 VKIADFGLS 168
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DB 170 VKIADFGLS 178

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RESULT 7
SNF1_CANGA
ID   SNF1_CANGA          STANDARD;          PRT:  61 AA.
AC   Q00472;
DT   01-MAY-1997 (Rel. 35, Created)
DI   01-MAY-1997 (Rel. 35, Last sequence update)
DI   15-JUN-1999 (Rel. 38, Last annotation update)
DE   Carbon catabolite derepressing protein kinase (EC 2.7.1. ).
GN   SNF1;
OS   Candida glabrata (Yeast) (Torulopsis glabrata).
OC   Eukaryota; Eukaryota; Ascomycota; Saccharomycetes.
OC   Saccharomycetes; Ascomycota; Saccharomycetes; Candida.
OX   NCBI_TaxID: 5478;
RN   [1]
RP   SEQUENCE FROM N.A.

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RE   STRAIN: NCCLS84;
RX   MEDLINE 97101019; PubMed 8945576;
RA   Pottier, R., Kwon-Chang, K.J.;
RT   "Disruption of the SNF1 gene abolishes trehalose utilization in the
RI   pathogenic yeast Candida glabrata.";
RL   Infect. Immun. 115:5269-5273(1998).
CC   1. FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT
CC   INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY
CC   PROTEIN SNF4. COULD PHOSPHORYLATES CAT8 (BY SIMILARITY).
CC   2. SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (BY
CC   SIMILARITY).
CC   3. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   SNF1 SUBFAMILY.
CC   -----
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (for http://www.ebi.ac.uk/ebis/ebis/
CC   or send an email to license@ebi.ac.uk).
CC   -----
DR   EMBL: L78130; AAM48642.1;
DR   HSSP: P03518; 2PHK;
DR   InterPro: IPR000719; Euk_pkinase;
DR   InterPro: IPR002290; Ser_thr_pkinase;
DR   Pfam: PF00069; pkinase_1;
DR   SMART: SM00220; S_TKc; 1;
DR   PROSITE: PS00167; PROTEIN_KINASE_ATP_1;
DR   PROSITE: PS00168; PROTEIN_KINASE_ST_1;
DR   PROSITE: PS00111; PROTEIN_KINASE_DOM_1;
KW   Transferase; Serine/threonine protein kinase; ATP-binding;
KW   Phosphorylation; Carbohydrate metabolism; Nuclear protein.
FT   DOMAIN      6   17    P-450-HIS.
FT   DOMAIN      75   292   FLUTIN KINASE.
FT   NP_BIND     45   55    ATP (BY SIMILARITY).
FT   BINDING     66   66    ATP (BY SIMILARITY).
FT   ACT_SITE    161   161   BY SIMILARITY.
FT   ACT_SITE    164   164   BY SIMILARITY.
FT   ACT_SITE    164   164   BY SIMILARITY.
SQ   SEQUENCE  611 AA;  70490 MW;  891791A4A900C0 CRR64;

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Query Match 1.7%; Score 9; DI 1; Length 611;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 160 VKIADFGLS 168
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DB 170 VKIADFGLS 180

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RESULT 8
SNF1_CANDR
ID   SNF1_CANDR          STANDARD;          PRT:  619 AA.
AC   Q94198;
DT   15-JUN-1999 (Rel. 38, Created)
DI   15-JUN-1999 (Rel. 38, Last sequence update)
DI   15-JUN-1999 (Rel. 38, Last annotation update)
DE   Carbon catabolite derepressing protein kinase (EC 2.7.1. ).
GN   SNF1;
OS   Candida tropicalis (Yeast).
OC   Eukaryota; Eukaryota; Ascomycota; Saccharomycetes.
OC   Saccharomycetes; Ascomycota; Saccharomycetes; Candida.
OX   NCBI_TaxID: 5478;
RN   [1]
RP   SEQUENCE FROM N.A.
PA   Kawai, T., Kawai, K., Kawai, M., Tanaka, A.;
RT   "Genetic evaluation of the function of SNF1 in Candida tropicalis.";
RL   J. Biol. Chem. 273:11111-11116(1998).
CC   1. FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT
CC   INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY
CC   PROTEIN SNF4. COULD PHOSPHORYLATES CAT8 (BY SIMILARITY).
CC   2. SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (BY

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RESULT 1 (1)
SNP1_YEAST
ID      SNP1_YEAST          STANDARD,          PRI;          333 AA
AC      P06782;
DE      01-JAN-1988 (Ref. 06, Created)
DT      01-JAN-1988 (Ref. 06, Last sequence update)
DL      15-MAR-1999 (Ref. 08, Last annotation update)
FE      Carbon catabolite derepressing protein Kinase (Ec 2.7.1.3).
GN      SNF1 OR CAT1 OR CCR1 OR PAS14 OR GLA2 OR YDR477W OR D8033.20.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Eumetazoa; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomycos
OX      NCBI_TaxID: 4932;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE 86289464; PubMed 374554;
RA      Celenza J.L., Carlson M.;
RT      "A yeast gene that is essential for release from glucose repression
RT      encodes a protein kinase.";
RI      Science 233:1125-1180(1986).
RH      [2]
RP      SUGGESTED FROM N.A.
RA      Dietrich F.S., Mulligan J., Allen R., Araujo K., Aviles E.,
RA      Berna A., Carpenter L., Chen L., Cherry J.H., Chung H., Duncan M.,
RA      Burdick Smith S., Hyman R., Kemp C., Lasker D., Low H., Lin D.,
RA      Macchiale D., Nakahara K., Hamada A., Cohen J., et al., Petri F.K.,

```

KA Roberts D., Schramm S., Schroeder M., Sjaogren T., Shroff N.,
 KA Winant A., Nelson M., Feinstein D., Davis R.W.,
 RL Submitted (Apr 1995) to the EMBL/Genbank/DBPRL Databases
 RN [4]
 RP SEQUENCE: F0274 DBL, 518 519 AA, (22 63), AND PHOSPHORYLATION SITE.
 KY MF0198: 9411998, PubMed 750477.
 KA Mitchell K.L., Stapleton J., Cao G., House C., Mitchell R.,
 KA Katsis E., Witters L.A., Kemp B.E.,
 RI "Mammalian AMP-activated protein kinase shares structural and
 RI functional homology with the catalytic domain of yeast Snf1 protein
 RI kinase." J. Biol. Chem. 269:2451-2454(1994).
 CC -1- FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT
 CC INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY
 CC PROTEIN SNF1. INTERACTS ALSO WITH SIPI, SIP2 AND GAL83. COULD
 CC PHOSPHORYLATES CAT8.
 CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC SNF1 SUBFAMILY.
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 CC -----
 DR EMBL: N13971; AAA5058.1; -.
 DR EMBL: H33070; AAB04904.1; -.
 DR PIR: A26030; A26030.
 DR RSDP: L62450; LA06.
 DR SIB: SIB02985; SNF1
 DR InterPro: IPR000719; Pak_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00229; SH2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transferase: Serine/threonine protein kinase; ATP-binding;
 KW Phosphorylation; Carbohydrate metabolism; Nuclear protein.
 FT DOMAIN 18 32 POLY-HIS.
 FT DOMAIN 55 306 PROTEIN_KINASE.
 FT NP_BIND 61 69 ATP (BY SIMILARITY).
 FT BINDING 84 84 ATP (BY SIMILARITY).
 FT ACT_SITE 177 177 BY SIMILARITY.
 FT MOTIF 210 210 PHOSPHORYLATION (AUTO).
 SQ SEQUENCE: 613 AA 72045 HW 15063565096414140964.

Query Match 1.7%, Score 9, DB 1, Length 533;
 Best Local Similarity 100.0%, Pred. No. 0.49;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 160 VKIADPGL 168
 |||||
 Db 191 VKIADPGL 199

RESULT 11

JAK3_HUMAN
 ID JAK3_HUMAN STANDARD: PRT: 1100 AA.
 AC Q66272;
 DI 01-NOV-1997 (Ref. 35, Created)
 DI 01-NOV-1997 (Ref. 35, Last sequence update)
 DI 16-OCT-2001 (Ref. 40, Last annotation update)
 DE Tyrosine protein kinase JAK3 (E.C. 2.7.1.12) (Janus kinase 3, JAK3).
 GN JAK3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurostomii; Muridae; Murinae; Rattus.
 OX NCBI_taxid 10116;

RN [1]
 RP SEQUENCE FROM NIA
 RC TISSUE: Spleen;
 RX NIDBID 94192919, F0274 DBL, 518 519 AA, (22 63), AND PHOSPHORYLATION SITE.
 KA Takahashi T., Shirasawa T.,
 RT "Molecular cloning of rat JAK3, a novel member of the JAK family of
 RI protein tyrosine kinases." FEBS Lett. 342:124-128(1994).
 RI "FUNCTION: TYROSINE KINASE. IT IS A NON-RECEPTOR TYPE INVOLVED IN
 CC THE INTERLEUKIN 2 AND INTERLEUKIN 4 SIGNALING PATHWAY.
 CC PHOSPHORYLATES STAT6, IRS1, IRS2 AND PI3K.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
 CC ASSOCIATED (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: TRANSCRIBED IN A VARIETY OF TISSUES INCLUDING
 CC SPLEEN, LUNG, KIDNEY AND INTESTINE.
 CC -1- DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS, THE SECOND ONE
 CC PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
 CC PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
 CC DOMAIN 1.
 CC -1- PIR: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4 (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES, JAK
 CC SUBFAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----

DR EMBL: D2850B; BAA05B08.1; -.
 DR RSDP: P11621; JAK3.
 DR InterPro: IPR000299; Rnd_4.1.
 DR InterPro: IPR000719; Pak_kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 2.
 DR SMART: SM00295; B41; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00219; Tyk2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 2.
 DE PROSITE: PS00001; SH2; PAF01_N001.
 KW Transferase: Tyrosine protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; Repeat.

FT DOMAIN 372 472 SH2 (ATYPICAL)
 FT DOMAIN 511 717 PR THIN_KINASE 1
 FT DOMAIN 810 1091 PR THIN_KINASE 2
 FT NP_BIND 824 832 ATP (BY SIMILARITY).
 FT BINDING 851 851 ATP (BY SIMILARITY).
 FT ACT_SITE 945 945 BY SIMILARITY.
 FT MOD_RES 978 978 PHOSPHORYLATION (ACID) (BY SIMILARITY).
 SQ SEQUENCE 1100 AA: 12256 MW: 10590094141014140964.

Query Match 1.7%, Score 9, DB 1, Length 1100;
 Best Local Similarity 100.0%, Pred. No. 0.89;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 150 VKIADPGL 167
 |||||
 Db 191 VKIADPGL 199

RESULT 12

JAK3_HUMAN
 ID JAK3_HUMAN STANDARD: PRT: 1124 AA

Hum. Genet. 1967;73: 79(2000).
 : FUNCTION: TYROSINE KINASE. IN THE MAPK1/ERK1/2 PATHWAY, INVOLVED IN
 THE INTERLEUKIN-2 AND INTERLEUKIN-4 SIGNALING PATHWAY.
 PHOSPHORYLATES STAT6, IRS1, IRS2 AND PI3K.
 : CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 tyrosine phosphate.
 : SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
 ASSOCIATED (BY SIMILARITY).
 : ALTERNATIVE SPLICING: 2 FORMS, 1/TAFK2/TAKE2 (TAFK,
 2/TAKE5/SPIR) ARE (SLOW GROWING) AND 3/TAKE4/TAKE4 (TAKE,
 4/TAKE5/SPIR) ARE PRODUCED BY ALTERNATIVE SPLICING. Isoform 1 may be
 defective as it lack some part of the kinase domain.
 : TISSUE SPECIFICITY: IN NK CELLS AND AIR NK LIKE CELL LINE BUT NOT
 IN RESTING T CELLS OR IN OTHER TISSUES. THE B-CHAIN IS MORE
 COMMONLY SEEN IN HEMATOPOIETIC LINES, WHEREAS THE B-AND-H FORMS
 ARE DETECTED IN CELLS BOTH OF HEMATOPOIETIC AND EPITHELIAL
 ORIGINS.
 : DOMAIN: ENCOMPASSES TWO TRANSFERKINERASE DOMAINS, THE SECOND ONE
 PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
 PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
 DOMAIN 1.
 : PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4.
 : DISEASE: DEFECTS IN TAK3 ARE A CAUSE OF RECESSIVE T-CELL
 NEGATIVITY. CHILD POSITIVE SEVERE COMBINED IMMUNODEFICIENCY (1 TO
 3000), A CONDITION CHARACTERIZED BY THE ABSENCE OF CIRCULATING
 MATURE T-LYMPHOCYTES AND NK CELLS, NORMAL TO ELEVATED NUMBERS OF
 NONFUNCTIONAL B-LYMPHOCYTES, AND MARKED HYPLASIA OF LYMPHOID
 TISSUES.
 : SIMILARITY: BELONGS TO THE TYK FAMILY OF PROTEIN KINASES, JAK
 SUBFAMILY.
 : SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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DR	EMBL:	D09607:	AAA19626.1;
DR	EMBL:	G16101:	AAG19226.1;
DR	EMBL:	G16102:	AAG50227.1;
DR	EMBL:	H57096:	AAZ50542.1;
DR	BSP:	P11362:	TPSK.
DR	MIM:	600173:	.
DR	MIM:	600802:	.
DR	InterPro:	IPR000299:	Band_4.1.
DR	InterPro:	IPR000719:	Euk_pkinase.
DR	InterPro:	IPR000980:	SH2.
DR	InterPro:	IPR001245:	Tyr_pkinase.
DR	Pfam:	PF00069:	pkinase; 2.
DR	SMART:	SM00295:	B41; 1.
DR	SMART:	SM00252:	SH2; 1
DR	SMART:	SM00219:	TyKc; 1
DR	PROSITE:	PS0107:	PROTEIN_KINASE_ATP; 1.
DR	PROSITE:	PS0109:	PROTEIN_KINASE_TYK; 1.
DR	PROSITE:	PS0111:	PROTEIN_KINASE_DOM; 2.
DR	PROSITE:	PS0111:	SH2_FALSE_NEG.
FW	Transferase:	tyrosine-protein kinase:	ATP binding; Phosphorylation;
FW	SH2 domain, Repeat:	Alternative splicing; Disease mutation; SH2	
FT	DOMAIN	875..475	SH2 (ATYPICAL).
FT	DOMAIN	521..781	PROTEIN KINASE 1.
FT	DOMAIN	822..1111	PROTEIN KINASE 2.
FT	RT_KINSE	828..846	ATP (BY SIMILARITY).
FT	BINDING	855..855	ATP (BY SIMILARITY).
FT	ACT_SITE	949..949	BY SIMILARITY.
FT	MOD_RES	980..980	PHOSPHORYLATION (AUTO.) (BY SIMILARITY)
FT	VARSPLIT	1071..1124	HELMKE/WARPSPQDQSPVALPQLDMWSSGSGVIRAI AIDPKGHSLSES SAAGASVSQSVWAWSPVTSRW
FT	VARSPLIT	1071..1121	HELMKE/WARPSPQDQSPVALPQLDMWSSGSGVIRAI AIDPKGHSLSES SCYSWDSDMGWPTVISRW

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RESULTS 13
JAK3_MOUSE
ID JAK3_MOUSE STANDARD: PRT: 129% AA
AC Q62147; Q61747; Q61746;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tyrosine protein kinase JAK3 (EC 2.7.1.12) (Janus kinase 3) (JAK-3).
GN JAK3
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCIT_L147310090
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE 94390920; PubMed 7518579;
RX Kane S.G., Reddy E.P.;
RT "JAK3: a novel JAK kinase associated with terminal differentiation of
RT hematopoietic cells ";
RL Oncogene 9:2415-2423(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN BACKGROUND X 12- P2, 11539E (Hwasu).
RX MEDLINE 95183774; PubMed 8605329;
RX Curdjak O.P., Berglund J.;
RT "Murine JAK3 is preferentially expressed in hematopoietic tissues and
RT lymphocyte precursor cells.";
RL Blood 87:415-416(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX STRAIN BACKGROUND:
RX MEDLINE 94294024; PubMed 8022486;
RX Withalm R.A., Silverman G.F., Miura O., Lai K.S., Cwik C., Liu E.T.

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1116 JENL
 RT "1. Cloned from the T146 human fibroblast cell line, interferon plus
 1117 2 and 4 in lymphoid and myeloid cells."
 1118 Nature 370:153-157 (1994).
 1119
 1120 1 FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN
 1121 THE INTERFERON 2 AND INTERFERON 4 SIGNALING PATHWAY.
 1122 1123 SIGNALING STATE, IKK1, IKK2 AND IKK3.
 1124 1125 CATALYTIC ACTIVITY: ATP + a protein tyrosine + H₂O = protein
 1126 tyrosine phosphate.
 1127 1128 SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
 1129 ASSOCIATED (BY SIMILARITY).
 1130 1131 ALTERNATIVE SPLICING: 1 (isoform 1), 2 AND 3; ARE
 1132 1133 LACATED BY ALTERNATIVE SPLICING.
 1134 1135 TISSUE SPECIFICITY: HIGHLY LEVELS IN THE THYMUS WITH
 1136 1137 MODERATE LEVELS IN BONE MARROW, SPLEEN, FETAL LIVER AND
 1138 1139 ADULT LIVER. VERY LOW LEVELS IN ADULT KIDNEY, LUNG,
 1140 1141 HEART, BRAIN AND LIVER.
 1142 1143 DOMAIN: 1 (DOMAIN 1) IN THE TRANSFERASE DOMAIN, THE SECOND ONE
 1144 1145 PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
 1146 1147 PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
 1148 1149 DOMAIN 1.
 1150 1151 ELM: TYROSINE KINASE-RELATED IN KIDNEY, 1, 2 AND 11-4.
 1152 1153 SIMILARITY: 1154 1155 IN THE FAMILY OF TYROSINE KINASES. SEE
 1156 1157 SIMILARITY.
 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836

11 VARIATION 1299 1299 SET PROBABLY A PHOTODIAPYLL-SPECIFIC WHORL
 12 (IN ISOPYRME 2 AND ISOPYRME 3)
 13 1-99 100% 0 ACTIVITY.
 14 A 1 (IN REP. 2).
 15 S 1 (IN REP. 3).
 16 G 1 (IN REP. 4).
 17 MERTINE (IN REP. 5).
 18 K 1 (IN REP. 6).
 19 A 1 (IN REP. 2 AND 3).
 20 R 1 (IN REP. 4).
 21 A 1 (IN REP. 5 AND 6).
 22 N 1 (IN REP. 3).
 23 I 1 (IN REP. 4).
 24 G 1 (IN REP. 2 AND 3).
 25 R 1 (IN REP. 4).
 26 S 1 (IN REP. 5).
 27 1299 AA 143114 MW: 115999600 (143114) 143114

Query Match: 1.00; Score: 0; DB: 1; Length: 1299;
 Best Local Similarity: 100.00; Pos. No. 0/0;
 Matches: 0; Conserved: 0; Mismatches: 0; Gaps: 0.

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11 REPEAT 7 14 1
 12 REPEAT 28 58 2
 13 REPEAT 39 19 6
 14 REPEAT 59 60 4
 15 SEQUENCE 74 AA: 7477 MW: 115929144 (143114) 143114

Query Match: 1.00; Score: 0; DB: 1; Length: 74;
 Best Local Similarity: 100.00; Pos. No. 0/0;
 Matches: 0; Conserved: 0; Mismatches: 0; Gaps: 0.

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DR PIR: D26952; D26952.
DR PIR: A26933; A26933.
DR InterPro: IIR001450; 4Fe4S_ferredoxin.
DR Pfam: PF0007; Icr4; 1.
DR PROSITE: PS00198; 4FE4S_FERREROXIN; 1.
KW Electron transport; Iron sulfur; Nitrogen fixation; Plasmid;
KW Complete proteome.
FT CONFLICT 62 62 1 -> 1 (IN REF. 2).
FT CONFLICT 97 97 1 -> 8 (IN REF. 2).
SQ SEQUENCE 98 AA; 10537 MW; 0201C1A92-54C2D8 CRC64;

Query Match 1.5%; Score 8; 18 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 RSPSLNLL 535
IIII,III
DI 33 RSPSLNLL 40

Search completed: May 14, 2002, 21:45:29
Job time: 329 sec



Query Match: 1.78; Score: 3; BK: 2; Length: 2;
 Best Local Similarity: 10.0%; Prod. No. 118;
 Matching by: Dissimilarity to: Mismatch: 0; Gaps: 0

A>Status: preliminary; translated from cDNA/EST/1980
A/Accession: AF067874
A/Feature: 1-555 bp, CDS: 1-511 bp, ORF: 170 aa, MW: 19.6 kDSS
A/Cross-species: Human: NM_013357, HMD: q192366, PIRNA:AAA47 (c), PID:q192367
A/Experimental source: brain
A/S-similarity: Calcineurin-dependent protein kinase; protein kinase heterlogy
A/Keyword: alternative splicing; ATP-calmodulin binding; phosphotransferase; serine
P48-296 domain; protein kinase; h.c.1.4; FINS
P48-56/heptone; protein kinase ATP-binding motif
E48-468/product; calipermin; status predicted: OSPS
P418-377/cationic; calmodulin binding; status predicted
P212/Active site: lys; status predicted

Query Match: 1 26; Score 9; Df: 1; Length: 469;
 Best Local Similarity: 100.0%; Pred. No.: 1.5;
 Matches: 9; Mismatches: 0; Indels: 0; Gaps: 0;

LD 178 KLADFLSK 186

RESULT 10
 B90100
 cys-regulated kinase 1, reported in *Gillardia theta*, eukaryote
 C:Species: nucleomorph *Gillardia theta*
 A:Ref: 1 nucleomorph: in the cytoplasmic nucleomorph of a eukaryotic endosymbiont
 (Date: 10 May 2001; Seq. processing: (Date: 10 May 2001; stat: (Date: 15 Jun 2001)
 C:Accession: B90100
 E:Domain: 51-230 aa, 1.097, 2001; Unpublished, H., Beaton, H., Penny, D., Penny, D.:
 Nature 410, 1097-1100, 2001
 A:Title: The highly reduced genome of an enslaved alga, nucleus.
 A:Ref: 1 nucleomorph: X 230 aa, 1.097, 2001
 C:Accession: B90100
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residue(s): 1-472 (100%)
 A:Cross references: CP:AF165818; N1:U13791554; FILE AAK30926.1; GSPPB-GN00150
 C:Genetics:
 A:Gene: kin(snr1)
 A:Map position: 1
 A:Genome: nucleomorph
 C:Superfamily: AMP-activated protein kinase, protein kinase homology
 C:Keywords: nucleomorph

Query Match: 1.7%, Score 9; DB 2; Length 472;
Best Local Similarity: 100.0%, Pr-1. No. 1.6;
Matches: 9; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY	160	VK1ADP31.S	168
DB	149	VK1ADP31.S	152

RESIDU: 11
 S59941
 serine/threonine-specific protein kinase (EC 2.7.1.37) BKIN2 - Barley (Hordeum
 C: Species: Hordeum vulgare (barley)
 C: Date: 15-Feb-1996 #sequence_revision 01 Mar 1996 #text_change 26-Feb-1999
 C: Accession: S59941
 C: Humpel, M.; Vico, G.; Carlinga, J.; Ecker, L.R.A.; Shewry, P.R.; Hall, N.J.
 Plant Mol. Biol. 27, 1235-1240, 1995
 A: Title: Differential expression of two barley DMP1-related protein kinase genes.
 A: Reference number: S59941, M01B:95284374
 A: Accession: S59941
 A: Status: preliminary
 A: Molecule type: mba
 A: Residues: 1-473 (aa)
 A: Cross reference: M9901:929548
 C: Genetics:
 A: Gene: BKIN2

Description

Adenylate cyclase catalyzes the formation of peptidyl serinephosphate or peptidyl threonine
 C/Superfamily: AMP-activated protein kinase; protein kinase homology
 C/Keywords: AMP, aminophosphotransferase, marine, cAMP, cAMP-specific, protein kinase
 E:1-145/Domain: protein kinase homology; *status: predicted
 E:1-145/1-117/Active site: Lys, Glu, Asp, Lys *status: predicted
 E:1-124/Domain: serine/magnesium (Asn, Asp) *status: predicted

Query Match: 100.00% Identity: 100.00% Length: 473
 Ref: 129.82ADP-1S-157
 Match: 100.00% Identity: 100.00% Mismatches: 0 Indels: 0 Gaps: 0

27 129.82ADP-1S-157

129.82ADP-1S-157

RESULTS

A:Accession: A41103
 C:Species: *Rattus norvegicus* (Norway rat)
 C/Date: 01-Mar-1994 #sequence revision 01-Mar-1994 #text change 11-Jun-1994
 C/Accession: A41103; A41247; A52865; A41250; A5335; A60255; 154706
 R:Ohmstedt, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.
 Proc. Natl. Acad. Sci. U.S.A. 88, 5784-5788, 1991
 A:Title: Relationship of gene encoding Ca(2+)-dependent protein kinase IV
 A/Reference number: A41103; M01091288548
 A/Accession: A41103
 A:Molecule type: DNA
 A:Residues: 47, 141, 144, 474 (OH1)
 A/Cross references: GB:024488; NID:q203219; PID:AAA40845.1; PID:q203220
 A/Note: This sequence has been revised in reference A41247
 A/Note: part of this sequence was confirmed by sequencing of cDNA to cKIN
 R:Ohmstedt, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991
 A/Reference number: A41247
 A/Accession: A41247
 A:Molecule type: DNA
 A:Residues: 142, 144 (OH2)
 A/Cross references: GB:M53334
 A/Note: this is a revision to the sequence from reference A41103
 R:Ohmstedt, C.A.; Jensen, K.F.; Sahyoun, N.F.
 J. Biol. Chem. 264, 5866-5875, 1989
 A:Title: Ca(2+)-calmodulin-dependent protein kinase enriched in cerebellar granule
 A/Reference number: A52865; M0109174647
 A/Accession: A52865
 A:Molecule type: mRNA
 A:Residues: 250, 474 (OH3)
 A/Cross references: GB:14660; NID:q203172; PID:AAA41862.1; PID:q203173
 R:Means, A.R.; Cruzalegui, L.; LeMaquerresse, B.; Needleman, D.S.; Slaughter, C.A.
 Mol. Cell. Biol. 11, 6967-6971, 1991
 A:Title: A novel Ca(2+)-calmodulin-dependent protein kinase and a male germ cell sp
 A/Reference number: A41250; M0109106487
 A/Accession: A41250
 A:Molecule type: mRNA
 A:Residues: 1, 371, 373, 473-498, 507, 410, 474 (MEA)
 A/Cross references: GB:M4457
 R:Oono, T.; Slaughter, C.A.; Cook, R.G.; Means, A.R.
 J. Biol. Chem. 264, 2081-2087, 1989
 A:Title: Molecular cloning, sequence and distribution of rat caldesmon, a non-tilin
 A/Reference number: A32045; M0109124272
 A/Accession: A32045
 A:Molecule type: mRNA
 A:Residues: 106, 371, 373, 474 (OH4)
 A/Cross references: GB:034445; NID:q203612; PID:AAA4090.1; PID:q203643
 R:Oono, T.; Means, A.R.
 Adv. Exp. Med. Biol. 255, 263-268, 1989
 A:Title: Caldesmon is a testis-specific calmodulin-binding protein closely related
 A/Reference number: A60255; M0109144189
 A/Accession: A60255
 A:Molecule type: protein
 A:Residues: 335, 369 (N2)
 A/Note: The amino end of caldesmon was blocked
 R:Bland, M.M.
 Gene 107, 351-352, 1993
 A:Title: Identification of alternate 5' untranslated regions in the gene on select
 A/Reference number: 154706; M0109131312
 A/Accession: 154706
 A:Status: preliminary, translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 (RES)
 A/Cross references: GB:116999; NID:q310036; PID:AAA17443.1; PID:q310087
 C/Comment: Ca(2+)-calmodulin-dependent protein kinase IV is enriched in cerebellar gran
 and in sperm cells.
 C/Superfamily: Ca(2+)-calmodulin-dependent protein kinase; protein kinase homology
 C/Keywords: alternative splicing; ATP, calmodulin binding; phosphotransferase
 E:40-296/Domain: protein kinase homology; *KIN

Query Match: 100.00% Identity: 100.00% Length: 473
 Ref: 129.82ADP-1S-157
 Match: 100.00% Identity: 100.00% Mismatches: 0 Indels: 0 Gaps: 0

27 129.82ADP-1S-157

129.82ADP-1S-157

E:48-57/Region: protein kinase ATP-binding motif
E:95-174/Region: calyculin A status predicted (CSP)
E:318-337/Region: calmodulin binding status predicted
E:71/Active site: lys status predicted

Query Match 1.7%; Score 9; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KIADEGLSK 169
IIIIIIII
DB 176 KIADEGLSK 186

RESULT 14
152637
Ca2+/calmodulin dependent protein kinase IV beta polypeptide - rat
C:Species: Rattus Sp. (rat)
C:Date: 26-Jul-1995 #sequence_revision 26 Jul 1995 #text_change 18-Jun-1999
C:Accession: 152637
R:Sakagami, H.; Kondo, H.
Brain Res. Mol. Brain Res. 19, 215-218, 1993
A:Title: Cloning and sequencing of a gene encoding the beta polypeptide of Ca2+/calmodulin
A:Reference number: 152637; MUID:94018484
A:Accession: 152637
A>Status: preliminary; Translated from GB/EMBL/DBSJ
A:Molecule type: mRNA
A:Residues: 1-503 <RES>
A:Cross-references: GB:5840; NIH:3425387; HDN:AAB29372.1; PID:q425384
C:Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
C:Keywords: ATP; calmodulin binding
E:68-724/Region: protein kinase homology <KIP>
E:76-84/Region: protein kinase ATP-binding motif

Query Match 1.7%; Score 9; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 KIADEGLSK 169
IIIIIIII
DB 206 KIADEGLSK 214

RESULT 15
116449
probably serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N:Alternate names: SNF1-related protein kinase
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16 Jul 1999 #text_change 29 Jul 2000
C:Accession: 116449
R:Campbell, N.J.
Submitted to the EMBL Data Library, December 1996
A:Reference number: 217020
A:Accession: 116449
A>Status: preliminary; Translated from GB/EMBL/DBSJ
A:Molecule type: mRNA
A:Residues: 1-501 <SUM>
A:Cross-references: EMBL:Y14036
A:Experimental source: cv. Masterpiece; cotyledon
C:Function:
A:Description: catalyzes the formation of peptide-serine phosphate or peptide-threonine
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
E:6-260/Region: protein kinase homology <KIN>

Query Match 1.7%; Score 9; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 VKIADFGLS 168

IIIIIIII
DB 141 VKIADFGLS 153

Search completed: May 14, 2002, 21:54:44
Job time: 658 sec

QY 168 VKIADPGLS 168
 11111111
 DB 16 VKIADPGLS 16

RESULT 1
 I49118
 link 76 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02 Jul 1996 #text_change 14-Sep-1996
 C:Accession: I49118
 R:Siyanova, E.Y.; Serfas, M.S.; Hazz, J.A.; Tyer, A.L.
 Mamm. Genome 5, 2053-2057, 1994
 A:Title: Tyrosine kinase gene expression in the mouse small intestine.
 A:Reference number: I49118; MUID:94268845
 A:Accession: I49118
 A:Status: preliminary, translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 166 <RES>
 A:Cross-references: EMBL:U13259, R11 3532777, 1 DBI AAB0447.1, F01454292
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology (fragment); K18
 F0166/Domains: protein kinase homology (fragment); K18

Query Match 1.7%; Score 9; DB 1; Length 168
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 168 VKIADPGLS 168
 11111111
 DB 16 VKIADPGLS 26

RESULT 4
 I48695
 gene nsk1 protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02 Jul 1996 #text_change 24-Sep-1996
 C:Accession: I48695
 R:Reith, A.D.
 Mamm. Genome 5, 689, 1995
 A:Title: Isolation and chromosomal location of Nsk1, a novel murine protein-tyrosine kinase.
 A:Reference number: I48695; MUID:96061159
 A:Accession: I48695
 A:Status: preliminary, translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 167 <RES>
 A:Cross-references: EMBL:X61457, R11 41 11665, 1 DBI AAB0127.1, F01454292
 C:Genetics:
 A:Gene: Nsk1
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology (fragment); K18
 F0167/Domains: protein kinase homology (fragment); K18

Query Match 1.7%; Score 9; DB 2; Length 167
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 168 VKIADPGLS 168
 11111111
 DB 17 VKIADPGLS 25

RESULT 5
 T29805
 hypothetical protein T25A8.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Jul-1999 #sequence_revision 15-Jul-1999 #text_change 14-Sep-2000
 C:Accession: T29805
 R:Latreille, P.; Stellyes, L.
 Submitted to the EMBL Data Library, June 1996
 A:Description: The sequence of C. elegans CDSW125A8.

A:Reference number: T20609
 A:Accession: T29805
 A:Status: preliminary, translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1416 <DNA>
 A:Cross-references: EMBL:U13146, F01454292, F01454292, F01454292, F01454292
 A:Experimental source: strain Bristol; N2; WormBase: WGS
 C:Genetics:
 A:Gene: CDSW125A8.5
 A:Map position: 4
 A:Strain: T29805, T29805, T29805, T29805, T29805
 C:Superfamily: protein-tyrosine kinase homology (fragment); K18

Query Match 1.7%; Score 9; DB 1; Length 1416
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 168 VKIADPGLS 168
 11111111
 DB 16 VKIADPGLS 26

RESULT 6
 T33827
 hypothetical protein T33827 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 14-Sep-2000
 C:Accession: T33827
 R:Miller, N.; Wamsley, P.
 Submitted to the EMBL Data Library, November 1999
 A:Description: The sequence of C. elegans T33827
 A:Reference number: T214.9
 A:Accession: T33827
 A:Status: preliminary, translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1417 <DNA>
 A:Cross-references: EMBL:AF17016, F01454292, F01454292, F01454292, F01454292
 A:Experimental source: strain Bristol; N2; WormBase: WGS
 C:Genetics:
 A:Gene: CDSW125A8.7
 A:Map position: 1
 A:Strain: T29805, T29805, T29805, T29805, T29805
 C:Superfamily: protein-tyrosine kinase homology (fragment); K18

Query Match 1.7%; Score 9; DB 1; Length 1417
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 168 VKIADPGLS 168
 11111111
 DB 16 VKIADPGLS 26

RESULT 7
 T33870
 hypothetical protein T33870 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 14-Sep-2000
 C:Accession: T33870
 R:Graves, P.; McDonald, R.
 Submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of C. elegans T33870
 A:Reference number: T21:78
 A:Accession: T33870
 A:Status: preliminary, translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1430 <DNA>
 A:Cross-references: EMBL:AF17016, F01454292, F01454292, F01454292, F01454292
 A:Experimental source: strain Bristol; N2; WormBase: WGS
 C:Genetics:
 A:Gene: CDSW125E7.10a



Query Match 36.1%; Score 195; DI 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 4.e-189;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 PILGICNEPFLGIVTEYMPNGLNELHKKTEYPDVWPLRFRILHEIALGVNYLHNM 139
Db 70 PILGICNEPFLGIVTEYMPNGLNELHKKTEYPDVWPLRFRILHEIALGVNYLHNM 129
Qy 140 PPLIHDLKTONILLDNEFHVKIADFLSKWRMMSLSRSSKSAPEGGTIYMPPE 199
Db 130 PPLIHDLKTONILLDNEFHVKIADFLSKWRMMSLSRSSKSAPEGGTIYMPPE 189
Qy 200 PGQSKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLIMYSVSGQHRPVINEESLPYDI 259
Db 190 PGQSKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLIMYSVSGQHRPVINEESLPYDI 249
Qy 260 PHFARMISLIESGWA 274
Db 250 PHFARMISLIESGWA 264

RESULT 10
US-09-069-023-6
; Sequence 5; Application US/09069023A
; Patent No. 6348571
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: NM-03333
; CURRENT APPLICATION NUMBER: US/09/069-023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-6

Query Match 36.3%; Score 167; DI 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.8e-161;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 SRKAQDCYFMKLIHHCPCGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLOP 433
Db 1 SRKAQDCYFMKLIHHCPCGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLOP 60
Qy 434 STALQWITKRPDIYNQSTEAFLNQLDALLSRDLINFEIYELVSTKPTRTSKVRQLD 493
Db 61 STALQWITKRPDIYNQSTEAFLNQLDALLSRDLINFEIYELVSTKPTRTSKVRQLD 120
Qy 494 IDICGEEFAKVIQKLNKQMLQPYEPLVVSRSISMLLONKSM 540
Db 121 IDICGEEFAKVIQKLNKQMLQPYEPLVVSRSISMLLONKSM 167

RESULT 11
US-09-099-041A-5
; Sequence 5; Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USE THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099-041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-05

; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-5

Query Match 20.6%; Score 111; DI 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-104;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

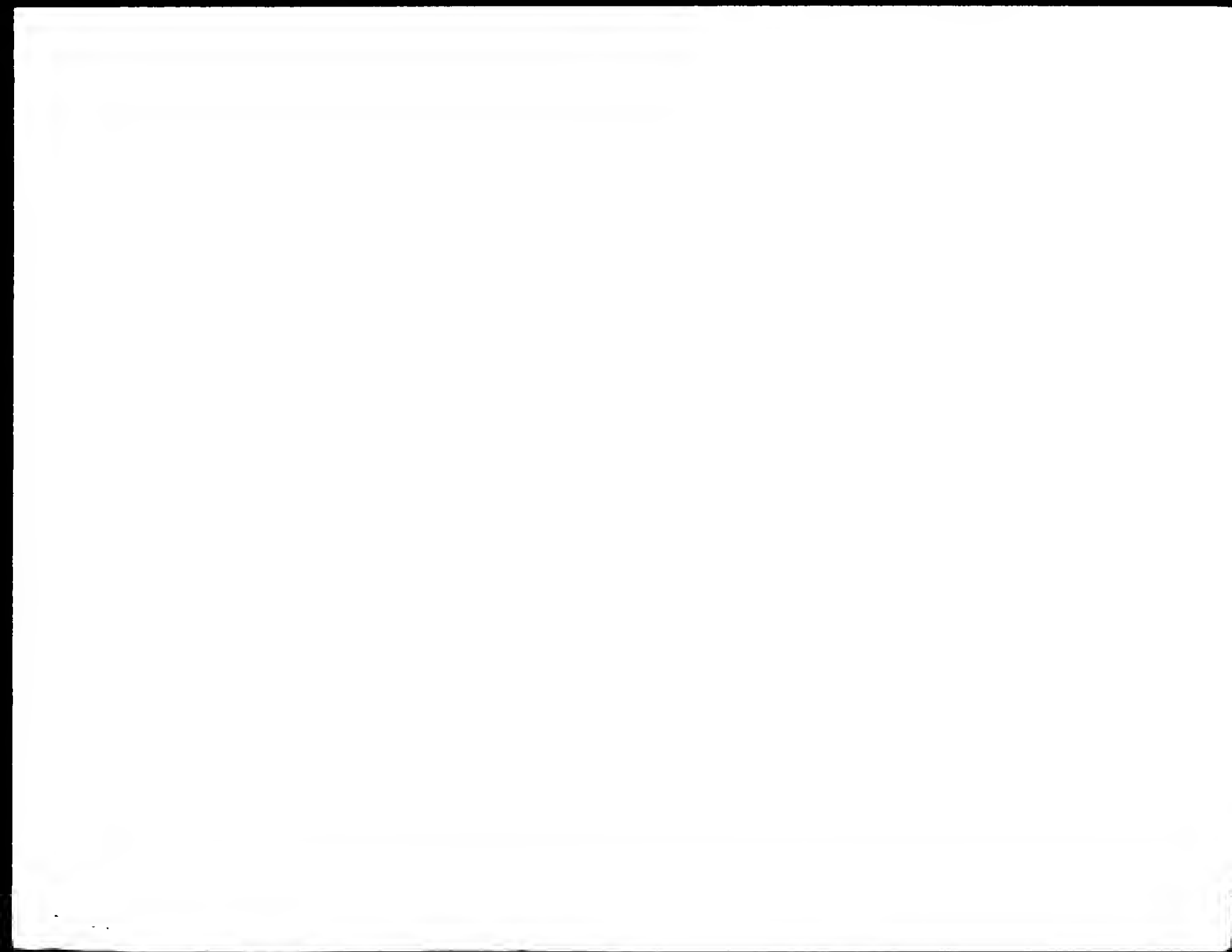
Qy 401 TPIKAVIQLEKTKIISVSSAIIHLEKKKMEISLNIPIVNUGQVNNPQVQLHDSGSPRT 460
Db 1 TPIKAVIQLEKTKIISVSSAIIHLEKKKMEISLNIPIVNUGQVNNPQVQLHDSGSPRT 60
Qy 361 SRSLPAPQNDPLSRKAQDCYFMKLIHHCPCGNHSDSTISGSQRAAFCDHKIT 411
Db 61 SRSLPAPQNDPLSRKAQDCYFMKLIHHCPCGNHSDSTISGSQRAAFCDHKIT 111

RESULT 12
US-09-099-041A-6
; Sequence 5; Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USE THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099-041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-099-041A-6

Query Match 20.2%; Score 109; DI 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.8e-102;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 QPGIAQWIDQKKEPTVQGMTHVNIHQSIHMLSRILIMPTVIVVSKPTRISKVRQL 493
Db 1 QPGIAQWIDQKKEPTVQGMTHVNIHQSIHMLSRILIMPTVIVVSKPTRISKVRQL 50
Qy 492 PSTRIGQTFPAKVIQKLNKQMLQPYEPLVVSRSISMLLONKSM 540
Db 61 PSTRIGQTFPAKVIQKLNKQMLQPYEPLVVSRSISMLLONKSM 167

RESULT 13
US-07-857-224B-25
; Sequence 25; Application US/0707857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) 80602
; COMPUTER READABLE FORM:



Tue May 14 08:27:48 2002

us-09-445-223-1.ra

Page 6

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-07-857-224B
FILING DATE: 03/25/92
CLASSIFICATION: 41b
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 18
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-25

Query Match 1.7%; Score 9; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 160 VKIADFGLS 160
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DB 139 VKIADFGIS 147

RESULT 14
US-08-701-191A-30
Sequence 10, Application US/08701191A
Patent No. 5,424,228
GENERAL INFORMATION:
APPLICANT: Moussa Mohammadi, Joseph Schlesinger,
APPLICANT: and Steven K. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NEW INVENTION RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 433 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2566
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-701,191A
FILING DATE: August 21, 1996
CLASSIFICATION: 530

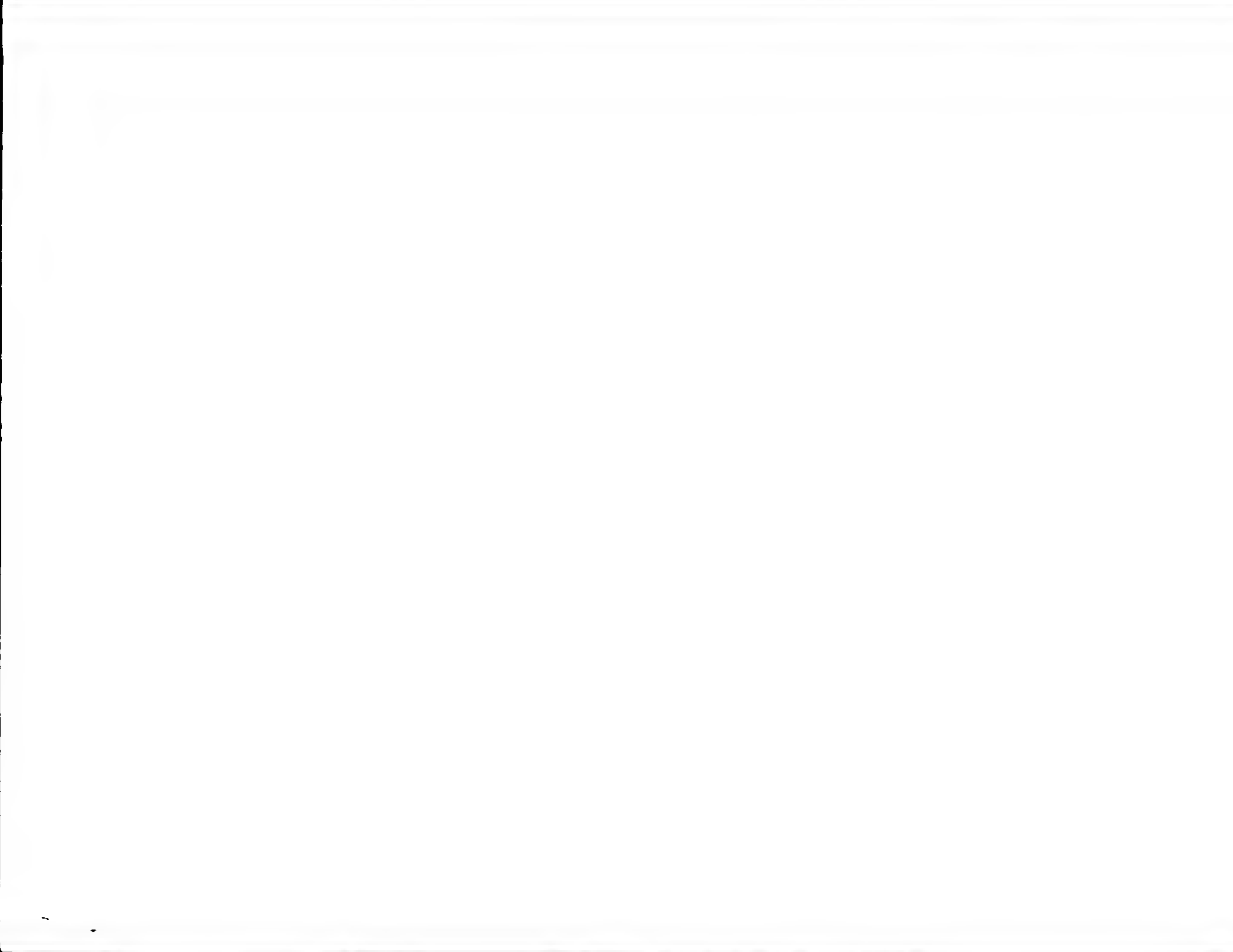
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 327,088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-701-191A-30

Query Match 1.7%; Score 9; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 160 VKIADFGLS 168
|||||
DB 178 VKIADFGLS 186

RESULT 15
PCT-US95-08493-2
Sequence 2, Application PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Caruso, Anthony
TITLE OF INVENTION: Novel alk Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT-US95-08493
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI5234A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08493-2

Query Match 1.7%; Score 9; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1



[illegible]

US-09-069-024-27

Query Match: 85.4%; Score 461; DB 4; Length 540;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 60 P L L G I C N E R E L L I V I E Y M F N S I N E L L H R K I E Y T V A W P L R F R I L H E I A L G V N Y L H N M T 139
 D6 60 P L L G I C N E R E L L I V I E Y M F N S I N E L L H R K I E Y T V A W P L R F R I L H E I A L G V N Y L H N M T 139

QV 140 P L L L H H D L K T N T I L N F P H V K I A N P I S K W M M S R Q S S S K S A P E S T I T Y M P P E N Y E 199
 D6 140 P L L L H H D L K T N T I L N F P H V K I A N P I S K W M M S R Q S S S K S A P E S T I T Y M P P E N Y E 199

QV 200 P L K P S A P I E H L Y F A V I W V L E F E L I T V I L L Q I R S V S Q G R F V I H E S L I Y R 279
 D6 200 P L K P S A P I E H L Y F A V I W V L E F E L I T V I L L Q I R S V S Q G R F V I H E S L I Y R 279

QV 260 P H P A P M I S I T S E W A L R P E R P S I K T I E L E V L I T E F I T I F A V I L E F I K I S V S S 319
 D6 260 P H P A P M I S I T S E W A L R P E R P S I K T I E L E V L I T E F I T I F A V I L E F I K I S V S S 319

QV 320 A D I C K K F M E I S I N I V S I P I L E S S A L I B E N I A I I S E S I C A P Q R H I S E K A Q 379
 D6 320 A D I C K K F M E I S I N I V S I P I L E S S A L I B E N I A I I S E S I C A P Q R H I S E K A Q 379

QV 380 C Y E K I H P C H N S W I T S I S L A A P C H Y T E R I A I N I S T A T S E R I Q S T A G W 439
 D6 380 C Y E K I H P C H N S W I T S I S L A A P C H Y T E R I A I N I S T A T S E R I Q S T A G W 439

QV 440 I L Q F E I V M L M E A L M S I A L I P H I M P L Q F I Y S E T E S E V R E L L T D T I Q G F 499
 D6 440 I L Q F E I V M L M E A L M S I A L I P H I M P L Q F I Y S E T E S E V R E L L T D T I Q G F 499

QV 500 P K A K V I Q R A K R K M S I Q V Y T I A V V R E S I L R K S M 540
 D6 500 P K A K V I Q R A K R K M S I Q V Y T I A V V R E S I L R K S M 540

RESULT 5
 US-09-019-942-1
 Sequence 1, Application US/09019942
 Patent No. 6440576

GENERAL INFORMATION:
 APPLICANT: Berlin, John
 TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
 TITLE OF INVENTION: DOMAIN POLYPEPTIDES
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/019,942
 FILING DATE: 06-FEB-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L.
 REGISTRATION NUMBER: 35,283
 REFERENCE TO OTHER DOCUMENTS: 07/04, 06/0001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 540 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MODIFIED TYPE: protein
 JS-09-019-942-1

Query Match: 86.7%; Score 360; DB 3; Length 540;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QV 60 P L L G I C N E R E L L I V I E Y M F N S I N E L L H R K I E Y T V A W P L R F R I L H E I A L G V N Y L H N M T 139
 D6 60 P L L G I C N E R E L L I V I E Y M F N S I N E L L H R K I E Y T V A W P L R F R I L H E I A L G V N Y L H N M T 139

QV 140 P L L L H H D L K T N T I L N F P H V K I A N P I S K W M M S R Q S S S K S A P E S T I T Y M P P E N Y E 199
 D6 140 P L L L H H D L K T N T I L N F P H V K I A N P I S K W M M S R Q S S S K S A P E S T I T Y M P P E N Y E 199

QV 200 P L K P S A P I E H L Y F A V I W V L E F E L I T V I L L Q I R S V S Q G R F V I H E S L I Y R 259
 D6 200 P L K P S A P I E H L Y F A V I W V L E F E L I T V I L L Q I R S V S Q G R F V I H E S L I Y R 259

QV 260 P H P A P M I S I T S E W A L R P E R P S I K T I E L E V L I T E F I T I F A V I L E F I K I S V S S 319
 D6 260 P H P A P M I S I T S E W A L R P E R P S I K T I E L E V L I T E F I T I F A V I L E F I K I S V S S 319

QV 320 A D I C K K F M E I S I N I V S I P I L E S S A L I B E N I A I I S E S I C A P Q R H I S E K A Q 379
 D6 320 A D I C K K F M E I S I N I V S I P I L E S S A L I B E N I A I I S E S I C A P Q R H I S E K A Q 379

QV 380 C Y E K I H P C H N S W I T S I S L A A P C H Y T E R I A I N I S T A T S E R I Q S T A G W 439
 D6 380 C Y E K I H P C H N S W I T S I S L A A P C H Y T E R I A I N I S T A T S E R I Q S T A G W 439

QV 440 I L Q F E I V M L M E A L M S I A L I P H I M P L Q F I Y S E T E S E V R E L L T D T I Q G F 499
 D6 440 I L Q F E I V M L M E A L M S I A L I P H I M P L Q F I Y S E T E S E V R E L L T D T I Q G F 499

QV 500 P K A K V I Q R A K R K M S I Q V Y T I A V V R E S I L R K S M 540
 D6 500 P K A K V I Q R A K R K M S I Q V Y T I A V V R E S I L R K S M 540

RESULT 6
 US-09-099-041A-2
 Sequence 2, Application US/09099041A
 Patent No. 6440576
 GENERAL INFORMATION:
 APPLICANT: Berlin, John
 TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 FILE REFERENCE: 07544-075001
 CURRENT APPLICATION: 09/099,041A
 CURRENT FILING DATE: 1998-06-17
 FILING APPLICATION NUMBER: 09/019,942
 PRIOR FILING DATE: 1998-02-06
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 540
 TYPE: PRO
 ORGANISM: Homo sapiens
 US-09-099-041A-2

Query Match: 86.7%; Score 360; DB 4; Length 540;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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> RESULT 9
> US 09/069,023-7
> Sequence 7, Application US/09/069,023A
> Patent No. 6,348,573
> GENERAL INFORMATION:
> APPLICANT: Nunez, Gabriel
> APPLICANT: Inohara, Naohiro
> APPLICANT: Koseki, Tsukuyoshi
> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
> TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
> FILE REFERENCE: DM-0333
> CURRENT FILING DATE: 1998-04-27
> CURRENT FILING DATE: 1998-04-27
> NUMBER OF SEQ. ID NOS.: 18
> SOFTWARE: Patent In Ver. 2.0
> SEQ. ID NO. 7
> LENGTH: 254
> TYPE: PRI
> ORGANISM: Homo Sapiens
> US 09/069,023-7

```

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: EINSUHL 14
: DS-07-857 224B-25
: Sequence 25, Application 95/07857/224B
: Patent No. 5958784
: GENERAL INFORMATION
: APPLICANT: Benner, Steven A.
: TITLE OF INVENTION: Predicting Folded Structures of Proteins
: NUMBER OF SEQUENCES: 114
: CORRESPONDENCE ADDRESS
: ADDRESSEE: Steven A. Benner
: STREET: Badlandsstrasse 151
: CITY: Zurich
: STATE: none
: COUNTRY: Switzerland
: Also referred to by an international patent code: GB-80/92
: COMPILED BY: A. B. L. R. M.

```

MEDIA TYPE: 3.5 inch diskette 1.44 MB storage
 OPERATING SYSTEM: Macintosh 7.0
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 02/02708493
 FILING DATE: 06/11/99
 CLASSIFICATION: 400

TELECOMMUNICATION DATA: none
 SEQUENCE INFORMATION:
 TELEPHONE: (International) 41-1-297-1800
 TELEFAX: (International) 41-1-297-2437
 TELEX: none

INFORMATION FOR SEQ ID NO: 05:

SEQUENCE CHARACTERISTICS:
 LENGTH: 257
 TYPE: amino acid
 STRANDEDNESS: none

MOLECULE TYPE:

DESCRIPTION: protein

ORIGIN: SOURCE:

ORGANISM: Saccharomyces cerevisiae

FEATURES: Protein Kinase; Table 10 Column 28

DESCRIPTION INFORMATION:

APPLICANT:

APPLICANT: Buckle, R. K.

APPLICANT: Smith, A. M.

APPLICANT: Hunter, L.

FIELD: The protein kinase family

DESCRIPTION:

LENGTH: 257

DATE: 1999

CLASSIFICATION: 25708493

Query Match: 1.7%, Score 9, ID 2, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 14

Query Match: 1.7%, Score 9, ID 3, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 15

Query Match: 1.7%, Score 9, ID 4, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

COMPUTER READABLE FORM

MEDIUM TYPE: 3.5 inch floppy, 1.44 MB

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 02/02708493

FILING DATE: 06/11/99

CLASSIFICATION: 400

TELECOMMUNICATION DATA: none

SEQUENCE INFORMATION:

TELEPHONE: (International) 41-1-297-1800

TELEFAX: (International) 41-1-297-2437

TELEX: none

TELECOMMUNICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICANT/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 42,427

REFERENCE/DOCKET NUMBER: 615,088

TELECOMMUNICATION INFORMATION:

TELEPHONE: (214) 489-1600

TELEFAX: (214) 955-0440

TELEX: 67 5510

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 304 amino acids

TYPE: amino acid

STRANDEDNESS: single

POPULOUS: linear

MOLECULE TYPE: protein

DESCRIPTION: 701-191A 40

Query Match: 1.7%, Score 9, ID 2, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 15

Query Match: 1.7%, Score 9, ID 3, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 15

Query Match: 1.7%, Score 9, ID 4, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 15

Query Match: 1.7%, Score 9, ID 5, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 15

Query Match: 1.7%, Score 9, ID 6, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 15

Query Match: 1.7%, Score 9, ID 7, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

160 VKIADPGLS 168

11111111

178 VKIADPGLS 186

RESULT 15

Query Match: 1.7%, Score 9, ID 8, Length 304;

Best Local Similarity: 100.0%, Prod. No. 0.52;

Matches: 9; Conservative: 0; Mismatches: 0; Gaps: 0;

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Page 7

Qy 160 VKIADFGLS 168
 |||||
Db 400 VKIADFGLS 408

Search completed: May 13, 2002, 21:33:40
Job time: 5726 sec



377
111
121

Query Match 36.1%; Score 195; DS 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 4.3;-189;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 PTLGICNEPEFLGIVTEYMPNGSLNELHRKTEYPOVAWPLRFRILHEIALGVNYLHNM 139
DB 70 PTLGICNEPEFLGIVTEYMPNGSLNELHRKTEYPOVAWPLRFRILHEIALGVNYLHNM 129
QY 140 PPLHLDKTONILLDNEFHVKIADPGLSKWRMMSLSQSRSSKSAPEGGTIYMPPEY 199
DB 130 PPLHLDKTONILLDNEFHVKIADPGLSKWRMMSLSQSRSSKSAPEGGTIYMPPEY 199
QY 200 PGOKSRASIFHDIYSYAVITWVFLSRKOPPEVDVTPNLCIMYSVSGQHRPVIINEESLPYDI 259
DB 190 PGOKSRASIFHDIYSYAVITWVFLSRKOPPEVDVTPNLCIMYSVSGQHRPVIINEESLPYDI 249
QY 260 PHRRMISLIESGWA 274
DB 250 PHRRMISLIESGWA 254

PLT 10
US-09-023-6
Sequence 5, Application US/09069023A
Patent No. 6348573
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/059,041A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
US-09-069-023-6

Query Match 30.9%; Score 167; DS 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 5.3e-161;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 SRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 433
DB 1 SRKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHKITPCSSAIINPLSTAGNSERLQ 60
QY 434 GIAQOWIQSKREDIVNQMTEACLNQSLDALLSKDLIMKFWRLVATKPTRTSKVRQLLD 493
DB 61 GIAQOWIQSKREDIVNQMTEACLNQSLDALLSKDLIMKFWRLVATKPTRTSKVRQLLD 420
QY 494 IDPQGRKFAKVYVCKLKDKNKQMLGFYPRHVVSRSLKMLLNKSM 540
DB 101 IDPQGRKFAKVYVCKLKDKNKQMLGFYPRHVVSRSLKMLLNKSM 167

RESULT 11
US-09-099-041A-5
Sequence 5, Application US/09099041A
Patent No. 6340576
GENERAL INFORMATION:
APPLICANT: Berger, Steven A.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USE THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 141
TYPE: PRT
ORGANISM: Homo sapiens
US-09-099-041A-5

Query Match 20.6%; Score 111; DS 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 2e-104;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 TEIFAVIQIKKTKIQSVSSAIRCCKKKMEISLNIPVNHGQPKESGGSFCHENFESPT 360
DB 1 TEIFAVIQIKKTKIQSVSSAIRCCKKKMEISLNIPVNHGQPKESGGSFCHENFESPT 60
QY 361 SRSPAPQDNDPISKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHK 411
DB 61 SRSPAPQDNDPISKAQDCYFMKLLHCPGNHSDSTISGSQRAAFCDHK 111

RESULT 12
US-09-099-041A-6
Sequence 6, Application US/09099041A
Patent No. 6340576
GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USE THEREOF
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-099-041A-6

Query Match 20.2%; Score 109; DS 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1e-102;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 IDPQGRKFAKVYVCKLKDKNKQMLGFYPRHVVSRSLKMLLNKSM 491
DB 1 IDPQGRKFAKVYVCKLKDKNKQMLGFYPRHVVSRSLKMLLNKSM 60
QY 492 IDPQGRKFAKVYVCKLKDKNKQMLGFYPRHVVSRSLKMLLNKSM 540
DB 61 IDPQGRKFAKVYVCKLKDKNKQMLGFYPRHVVSRSLKMLLNKSM 167

RESULT 13
US-07-857-224B-25
Sequence 25, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Berger, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Berger
STREET: Badlandstrasse 15
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code, 7R 8002)
COMPUTER READABLE FORM:



Tue May 14 08:27:48 2002

us-09-445-223-1.ra

Page 6

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: 08/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2410
TELEFAX: (International) 41 1 267 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 2;
PUBLICATION INFORMATION:
AUTHOR:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-51
DATE: 1988
US-07-857-224B-25

Query Match 1.7%; Score 9; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 VKIADFGLS 168
|||||||
139 VKIADFGLS 147

RESULT 14
US-08-701-191A-30
Sequence 30, Application US/08701191A
Patent No. 5942428
GENERAL INFORMATION:
APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Steven R. Haggard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: August 21, 1996
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-5440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-701-191A-30

Query Match 1.7%; Score 9; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 VKIADFGLS 168
|||||||
Db 178 VKIADFGLS 186

RESULT 15
PCT-US95-08493-2
Sequence 2, Application PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Caruso, Anthony
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0 Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08493
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15234A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08493-2

Query Match 1.7%; Score 9; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.61;



```

RESULT 1
AAW92795
ID AAW92795.1: Homo sapiens: F1: 7A.
EX
AC AAW92795:
XX
DE C7 RAT Bcl-2 (c11orf11)
XX
FE Homo F1 protein.
XX
FW Bcl protein, intracellular mediator of inhibitor of tumorigenesis cell death
FW cell survival pathway, intracellular dipolizer, AIDS: cancer: human,
XX
OS Homo sapiens.
XX
PN W08855507 A2.
XX
PO 10 DEC-1998.
XX
PR 01 JUN-1998: 98w01100255.
XX
PR 11 SEP-1997: 9711.0121746.
PR 05-JUN-1997: 9711.0121011.
PR 10 JUN 1997: 9711.0121199.
XX
FA (YF0A ) YF0A RES & REV 20 L110.
XX
FI Boldin M, Baltimore K, Wallach D:
XX
NA W011795.1: 258/06.
XX
FE Bcl-2b, AAW92795.
XX
FE Bcl protein, initiator cell death and cell survival pathways
PI derivatives, DNA and antibodies, also regulate intracellular

```

Query Match: 85.4%; Score 461; DB Cl: Length 478;
Best Local Similarity: ID:ID6; Pred No: 0;
Matches: 44; Deletions: 0; Mismatches: 0; Indels: 0; Gaps: 0

[illegible]

[illegible]

disorders, immune disorders and neuronal disorders. The FUSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with increased FUSP expression/activity. FUSP antagonists are useful for treating or preventing disorders associated with increased FUSP expression/activity.

ΔU ΔH ΔA ΔG

Query Match: 85.4%; Score: 461; ID: 21; Length: 540;
 Best Local Similarity: 100.0%; Prod. No.: B;
 Matches: 461; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

[illegible]

KISHIMOTO 5

 $\Delta \Delta H_4^{\circ} = 11.7 \text{ kJ mol}^{-1}$

ID: AAB4 1370 standard: Protein: 3rd AA

XX

$$A^{\circ} \quad \Lambda\Lambda B4 \quad 1^{\circ}, 7(0);$$

XX

19P FEB 2001 (first entry)

XX

11. Human cancer-associated protein sequence SKy. In No. 1115.

XX

KW Human: cancer-associated genes; cancer antigen; detection; cancer;
KW diagnosis; neoplasia; proliferative; vulnery; immunomodulation;
KW antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
KW antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
KW dermatological; immunoprotective; thrombolytic; coagulant; modulator;
KW vasopressor; antiproliferative; immunoprotective; immunoprotective;
KW immune disorder; hematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW hematological; thrombolytic; cardiovascular disorders; infectious;
KW neurological disorders; drug screening;

US Home Savings

XX

IN $W(20)(0^{1,5}3^{11}) \cdot A$.

XX

DOI: 10.1002/sep.20000

XX

PF 08-MAR-2000; 2000W-030502L
 XX
 PR 12-MAR-1999; 600S-012470
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA; Rubin SM;
 XX
 DE WP1; 1999 43269/41;
 DE N ISDB; AAC77777;
 XX
 PT Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer -
 XX
 PS Claim 11: Page 1595-1597; 2352pp; English.
 XX
 CC AAC77747 to AAC78449 encode the human cancer associated proteins either
 CC in AAB44359 to AAB44229. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC includes: cytostatic, proliferative, vascular, immunomodulator,
 CC antiinfective, antisthmatic, antirheumatic, antiatherosclerotic,
 CC antiinflammatory, antihypertensive, antifibrotic, antiviral,
 CC dermatological, neuroprotective, cardiac, thrombolytic, coagulant,
 CC neoplastic, vasotropic, antiproliferative and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for prevention, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of hematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44249 represent sequences used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 544 AA:

Query Match 85.4%; Score 461; DB 21; Length 544;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 PTLCTQNEPFLGIVTHYMNGSLNLLHKKLYPEVAVPLRIRILHEDIALGVRYLHMT 139
 Db 84 ptlctnepeflgltvtympnslgllhcklypdauplrrilrhelalgvrylhm 143
 Qy 140 LPLMHDLKLTQNTLIDNIEPVKTADELGSKWMMSLSGSRSSKSAFEGGTIIYMPENYE 199
 Db 144 pplthldkltqntlidniepvktdelgskwmmslsgsrssksafeggtiympep 203
 Qy 200 PDLGSRASIKHDLISYAVITWEVLSKQPFIDVINPQITMYSVSGHRRPVNFES 259
 Db 204 pldgsraskhdygavitwvlskqpfidvinpqltmysvsgahrrpvnfesl 263
 Qy 260 PIPARMISLIESWAGNIDERMSELKGLIFEPVLTFFERITILEAVIQLKRIKLGVSVS 319
 Db 264 piparmislieswagndermselekglifepvltfferitileavilgkklkgvss 323
 Qy 320 ALHLCDKKYKVLSTNIVNIDLPFFSGSLIHNFSNPTFRRIAPDNPFFPAG 379
 Db 324 alhlcdkkykvlstnivnidlpffsgslhfnfsnptfrriapdnppfpag 383
 Qy 380 CYFMKLHICPCHHSWDSIDSGRAAFQDITTPGSAINCLSTAGNSIKRQPTAQW 439
 Db 384 cyfmklhicpchkswdsidsgraafdkittpgsainclstagnsikrqpdaqw 443
 Qy 440 LQYKFFPVAVNMTACIKQVILACIIPGICRRIEYIVSVLEFTEIKVEQIDIT 499
 Db 444 lqskredvnpvteardcpdlfllrslldkldpqlskkplrksknplldlqk 503

Qy 500 LQYKFFPVAVNMTACIKQVILACIIPGICRRIEYIVSVLEFTEIKVEQIDIT 549
 Db 504 lqskredvnpvteardcpdlfllrslldkldpqlskkplrksknplldlqk 544

RESULT 6
 AAY31140
 ID AAY31140 standard; Protein: 549 AA;
 AX
 AC AAY31140;
 XX
 DT 25-OCT-1999 (first entry)
 XX
 DE Human CARD-3 protein.
 XX
 KW CARD-3; caspase recruitment domain; CARD-4; regulation; detection;
 KW caspase activation; detection; screening; therapy; diagnosis; disease;
 KW apoptosis; cell death; Fas/FasL receptor complex; TNF receptor complex;
 KW cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection;
 KW hormone dependent tumor; autoimmune disorder; Alzheimer's disease;
 KW systemic lupus erythematosus; immune mediated glomerulonephritis; stroke;
 KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
 KW spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;
 KW myotubular syndrome; myocardial infarction; cell proliferation;
 KW cell differentiation; cell survival; CARD 3L; CARD 4S; CARD 4Y;
 XX
 OG Homo sapiens.
 XX
 FE Feature/Qualifiers
 FT Domain 1..300
 FT Note "predicted kinase domain"
 FT Domain 301..431
 FT Note "predicted linker domain"
 FT Domain 432..549
 FT Note "predicted CARD domain"
 XX
 PN W09941102-A1.
 XX
 ID 12 AUG-1999.
 XX
 DE 05-FEB-1999; 90WP-0802544
 XX
 PR 08 DEC-1998; 98US-0207459.
 PR 06-FEB-1998; 98US-0019942.
 PR 17 JUN-1998; 98US-0099041.
 XX
 PA (HUMA-) MILLERTRUB PHARM INC.
 XX
 PI Berlin J;
 XX
 DE WP1; 1999 43269/41;
 DE N ISDB; AA209246
 XX
 PT Novel CARD-3 and CARD-4 genes and polypeptides used or treating
 PT regulation of cellular proliferation and differentiation and cell
 PT survival
 XX
 PS Example 2; Fig. 2; 181pp; English.
 XX
 CC This invention describes the isolation of novel human caspase
 CC recruitment domain (CARD-3 and CARD-4) genes and proteins and a
 CC partial murine CARD-4 protein and genes. The genes and proteins of
 CC the invention are used in the regulation of caspase activation.
 CC The caspase recruitment domain (CARD) polynucleotides, polypeptides,
 CC liposomes and antibodies can be used in screening assays, detection
 CC assays, predictive medicine and therapeutic and prophylactic methods of
 CC treatment. The methods may be used to diagnose and treat patients which
 CC are suffering from a disorder associated with abnormal level or rate of
 CC apoptosis, cell death, ataxia, etc., or the Fas/FasL receptor
 CC complex, abnormal activity of the TNF receptor complex, or abnormal
 CC activity of a caspase. The disorder may be treated in humans or
 CC (particularly follicular lymphoma, carcinomas associated with mutations

in post-natal hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosus, immune-mediated glomerulonephritis), viral infections (e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar degeneration, anemias, myelodysplastic syndrome, myocardial infarction, and stroke). CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation, and cell survival. The CARD proteins may also be used to screen drugs or compounds which modulate their activity. The CARD-4 gene can express a long transcript that encodes CARD-4L, a short transcript that encodes CARD-4S, or two CARD-4 splice variants, CARD-4Y and CARD-4Z. This sequence represents the human CARD-3 protein described in the method of the invention.

XX Sequence: 540 AA

Query Match: 66.7% Score: 360; DB: 22; Length: 540;
Best Local Similarity: 99.8%; Prol. No.: 9;
Matches: 460; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 80 EHTATGKPEPTIVTLYMFKKNTLTHKKTYTVDVAWLEKPTLHHTALGVNYLHRI 139
DB 80 pLHtGKPEPTIVTLYMFKKNTLTHKKTYTVDVAWLEKPTLHHTALGVNYLHRI 139
QY 140 PHLHHHLEFQNLHFNHVKIAEFGSEWMMSTSSSSSKSAPEGGTLYMPGAYVE 199
DB 140 pLHtHHHLEFQNLHFNHVKIAEFGSEWMMSTSSSSSKSAPEGGTLYMPGAYVE 199
QY 200 PTKKSLASTKHDIYSYAVITWEVLSKKQPEEDVNIHQIMYSVSGHHPVINEPSIDYD 259
DB 200 pTKKSLASTKHDIYSYAVITWEVLSKKQPEEDVNIHQIMYSVSGHHPVINEPSIDYD 259
QY 260 PHFARMSTLIESQWQNPDEKPSLTKLLEFVERITETELKAVIQLEKIKIQSVSS 319
DB 260 pHFARMSTLIESQWQNPDEKPSLTKLLEFVERITETELKAVIQLEKIKIQSVSS 319
QY 320 AIDHSTKFKKMLNTHFYNHPELQYVNLQHNLNTHPEISLAPLNHHLKRAQ 379
DB 320 AIDHSTKFKKMLNTHFYNHPELQYVNLQHNLNTHPEISLAPLNHHLKRAQ 379
QY 380 AHHKLTGKPNSSWDTLHSGQAARLQKLTSSSAITNPTSTAGNSERQDPTAQGW 439
DB 380 AHHKLTGKPNSSWDTLHSGQAARLQKLTSSSAITNPTSTAGNSERQDPTAQGW 439
QY 440 LSKRPTVYKHETANTNCHFAVETREIKKLYTLYWSTPEIKSKVAGLHHTDTPH 499
DB 440 LSKRPTVYKHETANTNCHFAVETREIKKLYTLYWSTPEIKSKVAGLHHTDTPH 499
QY 500 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 500 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

QY 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540
DB 540 LAKVLEKRLNKKMLGQPTLEAVVDTLHNTLQHRM 540

E1 Domain: 1,400
E1 Note: "kinase domain"
E1 Domain: 401,431
E1 Note: "linker domain"
E1 Domain: 432,540
E1 Note: "CARD"

FN W020100826-A2

FN 04-JAN-2001

FI 28-JUN-2000; 2000W0-0517591

FI 28-JUN-1999; 1999S-0340620

IA (MILL.) MILLENNIUM PHARM INC.

FI Berlin JE

DB WPI, 2001 061974/07

DB NPSDB; AAF0001

FI Isolated intracellular proteins predicted to be involved in regulating caspase activation are used for diagnosis and treatment of cancer, viral infections, autoimmune diseases, neurological diseases and haematological disorders.

PS Claim 9; Fig. 2; 20pp; English

CC The present sequence is that of human caspase recruitment domain-3 (CARD-3), an intracellular protein predicted to be involved in regulating caspase activation. The sequence is predicted from an isolated cDNA clone (see AAF0001). Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal level or rate of apoptotic cell death, abnormal activity of the Fas/CARD-1 receptor complex, abnormal activity of the tumour necrosis factor receptor complex or abnormal activity of a caspase (e.g. by administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CARD-6 or a fusion gene therapy methods. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD-3, CARD-4, CARD-5 and CARD-6 proteins can be used to regulate cell proliferation, cell survival and cell growth. They can also be used to screen drugs or compounds that modulate their activity or expression and to treat disorders associated with insufficient or excessive production of CARD-3, CARD-4, CARD-5 or CARD-6 protein, or production of an aberrant protein.

XX Sequence: 540 AA

Query Match: 66.7% Score: 360; DB: 22; Length: 540;
Best Local Similarity: 99.8%; Prol. No.: 9;
Matches: 460; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 80 EHTATGKPEPTIVTLYMFKKNTLTHKKTYTVDVAWLEKPTLHHTALGVNYLHRI 139
DB 80 pLHtGKPEPTIVTLYMFKKNTLTHKKTYTVDVAWLEKPTLHHTALGVNYLHRI 139
QY 140 PHLHHHLEFQNLHFNHVKIAEFGSEWMMSTSSSSSKSAPEGGTLYMPGAYVE 199
DB 140 pLHtHHHLEFQNLHFNHVKIAEFGSEWMMSTSSSSSKSAPEGGTLYMPGAYVE 199
QY 200 PTKKSLASTKHDIYSYAVITWEVLSKKQPEEDVNIHQIMYSVSGHHPVINEPSIDYD 259
DB 200 pTKKSLASTKHDIYSYAVITWEVLSKKQPEEDVNIHQIMYSVSGHHPVINEPSIDYD 259
QY 260 PHFARMSTLIESQWQNPDEKPSLTKLLEFVERITETELKAVIQLEKIKIQSVSS 319
DB 260 pHFARMSTLIESQWQNPDEKPSLTKLLEFVERITETELKAVIQLEKIKIQSVSS 319
QY 320 AIDHSTKFKKMLNTHFYNHPELQYVNLQHNLNTHPEISLAPLNHHLKRAQ 379
DB 320 AIDHSTKFKKMLNTHFYNHPELQYVNLQHNLNTHPEISLAPLNHHLKRAQ 379

CC media, and for diagnostically measuring RICK levels. A specific inhibitor
CC of an essential step in the biochemistry of apoptosis is needed. RICK
CC interaction with intracellular factors such as CLAP and PAR6 appears to
CC be essential for apoptosis. Inhibitors of RICK binding to intracellular
CC apoptosis factors are potential drug candidates.
CC Note: This sequence was created using information given in the
CC specification.
CC
XX
SO Sequence 284 AA:

```

Query Match      52.6%, Spine 284; DB 21; Length 284;
Best local Similarity 100.0%, Ident. No. 1, 4e-284;
Matches 284; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 YTHPHARMISLSYPSWAGNPNENRPHFLKELIENHVIPTFRGITILEAVYQLEKTKLQS 316
Db      | ythpharmislicswagndpnsfkkllnqepvtrfcdltlrcavqtkkklqs 60

Qy 376 YVSAAGMGLRLEHRLFLHLYVTHGQHTWPSYVQIHNGSGDPSSEKIPAPGNPKSRK 376
Db      | ysaahfndkkkksfslpshqhpqpsasaqihusagpotskllpapgndtlsrk 120

Qy 477 AGQCYFRKRLHRLYTHSKWRLSDAGKALSLHSLTFLHESALNFIYACGSSNPQSLA 476
Db      | agqcyfknllhqpshhzwsltsagsgaaafcdlktlpsallhpslagnsrllpqla 180

Qy 497 QWALNRPFLKDRKSLKLYLWALSKRLNPSLYLYLALPTTFYVQQLDITDI 496
Db      | qwalnqskredyhlplcarngsdalrlltsskndyglwklgpllskrlrlrlrtdl 240

Qy 549 QKSLFAYVPSYFTRQMTLHLPPTVVVSPSLHNGKSM 549
Db      | qkslfsayvpsyfrqmtlhlpptvvvssplhngksm 284

```

```

RESDUITS 9
AAM93621
ID AAM93621 standard; protein: 540 AA.
XX
AC AAM93621.
XX
DI 06-Nov-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 3454.
XX
KW human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EF140094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-MAR-2000; 2000EP-0114089.
XX
PR 08-JUN-1999; 1999P-0144486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000MP-0181764.
XX
PA (HELI-) HELIX RES UNS.
XX
PI Chai L, Nishikawa T, Inanaga E, Haseguchi E, Ichio S, Kawai Y,
PI Wakamatsu A, Nishiyama T, Maeda E, Kojima S, Haseguchi T, Koda K:
XX
WI: 2001-524351/58.
DE N-PSUB; AAK94554.
XX
XX
PT 830 primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation.
XX
PS Cloning B; SEQ ID NO 3454; 1800pp + sequence listing; English.
XX

```

51 The invention relates to primers for synthesising full length cDNA
 52 clones. cDNA molecules encoding a human protein have been
 53 isolated and nucleotide sequences of 5' and 3' ends of the cDNA
 54 sequences have been determined. Primers for synthesising the full length
 55 cDNA are useful for clarifying the function of the protein encoded by
 56 the cDNA. The full length clones were obtained by construction of full
 57 length cDNA libraries that were synthesised by the chain-extended
 58 method. The primers enable the production of the full length cDNA easily
 59 without any special methods. The present sequence is a polypeptide
 60 encoded by a full length human cDNA of the invention.
 61 Notes: the sequence data for this patent did not form part of the printed
 62 publication, but was obtained in CD ROM format directly from EPO.
 63
 64 Sequence: 167 AA.

Query Match: 30.9% Score: 255; DB: 22; Length: 540;
 Best Local Similarity: 100.0%; Pred. No.: 1; Gaps: 252;
 Matches: 167; Conservative: 0; Mismatches: 27; Indels: 0; Gaps: 0;

65 80 TTTGTCNFTFGLVIVYKMGNSNELTRKTKYDVAWPLRTRILRLTALGVNYLHMT 139
 66 TTTGTCNFTFGLVIVYKMGNSNELTRKTKYDVAWPLRTRILRLTALGVNYLHMT 139
 67 80 ptttgnftfglvivykmngnsneltrktkydvawplrtrilrltalgvnylhmt 139
 68 140 TPTTHHDKTONTLHHHTHVEIALFHTFWLHNGRLKSHKSEKALITETLYNELLRYL 199
 69 TPTTHHDKTONTLHHHTHVEIALFHTFWLHNGRLKSHKSEKALITETLYNELLRYL 199
 70 140 pttthhdktpntlhhhtthveialfhtfwlhngrlkshksekalitetlynellryl 199
 71 200 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 259
 72 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 259
 73 200 ptkrakrrhsysyavitwevlskkqfeeavnplqimysvsgrrivnhesleyl 259
 74 260 TLAALMLTTPSWANLHRLRTRKTLTPELVHETLETHHFAVLEKKIKESVSS 319
 75 TLAALMLTTPSWANLHRLRTRKTLTPELVHETLETHHFAVLEKKIKESVSS 319
 76 260 tlaalmlttpswanlhrlrtrkrtltpelvhethethhfavlekkikesvss 319
 77 320 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 379
 78 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 379
 79 320 ptkrakrrhsysyavitwevlskkqfeeavnplqimysvsgrrivnhesleyl 379
 80 400 CYMKLHHTPNNRWGHTLNLGAAAFIDKTLTVAIINPLTFAHSTPLGGTALQW 459
 81 CYMKLHHTPNNRWGHTLNLGAAAFIDKTLTVAIINPLTFAHSTPLGGTALQW 459
 82 400 cymklhhtpnnrwgghtlnlgaaafidkrtltpvaiinpltpahstplggtaalqw 459
 83 460 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 499
 84 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 499
 85 460 ptkrakrrhsysyavitwevlskkqfeeavnplqimysvsgrrivnhesleyl 499
 86 520 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 540
 87 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 540
 88 520 ptkrakrrhsysyavitwevlskkqfeeavnplqimysvsgrrivnhesleyl 540

RESULT 10
 AAY58948
 1 AAY58948 standard: Protein: 167 AA
 2
 3 AAY58948
 4
 5 21 MAR 2001 (first entry)
 6
 7 Human RICK protein sequence residues: 305-541
 8
 9 RICK: human RIP-like interacting (RIAP) kinase; apoptosis regulator; ARK;
 10 caspase-8, caspase-10, CD95 signalling; apoptosis signalling pathway;
 11 C10orf4; C10orf4; DRBP-1; diagnosis; cell growth; apoptosis dysregulation;
 12 gene therapy; metabolic disorder; cancer; neurodegenerative disorder; AIDS;
 13 apoptosis; necrosis; ischaemic injury; toxin-induced liver disease.
 14
 15 11 Dec 2000
 16
 17 W: 000141 A2
 18
 19

10 04 NOV 1999.
 11
 12 27 APR 1999; 99WO/US09103.
 13
 14 27 APR 1998; 98DS/069023.
 15
 16 (HRI) ; HIV MURKIN.
 17
 18 Numez C, Inohara N, Koseki T;
 19
 20 WPI; 2000 072164/06.
 21
 22 Compositions for identifying apoptosis signalling pathway inhibitors
 23 useful for treating diseases
 24
 25 Claim 5; Page: 1; 9pp; English.
 26
 27 This sequence is a fragment of the human RICK (RIP-like interacting (RIAP)
 28 kinase) protein of the invention. RICK acts as a positive regulator
 29 of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10
 30 during CD95 signalling. The invention provides methods for identifying
 31 apoptosis signalling pathway inhibitors and activators, and methods and
 32 compositions for screening compounds which will modulate the interactions
 33 of the various compositions identified: ARK, RICK, and the C10E family of
 34 activators (C10E-A, C10E-B and C10E-1). RICK is useful in screening
 35 assays for agents, useful in the diagnosis, prognosis or treatment of
 36 disease associated with excess cell growth and dysregulation of
 37 apoptosis. Complexes containing RICK and RIAP can be used in drug
 38 screening assays to identify inhibitor molecules blocking CD95-mediated
 39 apoptosis. Overexpression of ARK in an in vitro cell system can be used
 40 to identify inhibitors of the enzymatic activity of caspase-8.
 41 Identification of ARK-like inhibitory compounds may be useful for gene
 42 therapy treatment of disease with increased cell death in muscle disease
 43 and cardiac disorders. Therapeutic compositions of C10Es can be used to
 44 treat a wide range of AIDS, neurodegenerative disorders, aplastic anaemia,
 45 ischaemic injury, and toxin-induced liver disease. Anti-RICK antibodies
 46 can be used as reagents for the preparation of affinity chromatography
 47 media, and for diagnostically measuring RICK levels. A specific inhibitor
 48 of an essential step in the biochemistry of apoptosis is needed. RICK
 49 interaction with intracellular factors such as RIAP and FADD appears to
 50 be essential for apoptosis. Inhibitors of RICK binding to intracellular
 51 apoptosis factors are potential drug candidates.
 52 Notes: this sequence was created using information given in the
 53 specification.
 54
 55 Sequence: 167 AA.

Query Match: 30.9% Score: 167; DB: 11; Length: 167;
 Best Local Similarity: 100.0%; Pred. No.: 2; Gaps: 163;
 Matches: 167; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

56 371 TFEALITTFMFLHRTTDLKWLITLSLFAAPNTRKTLTVAIINPLTFAHSTPLGGTALQW 430
 57 TFEALITTFMFLHRTTDLKWLITLSLFAAPNTRKTLTVAIINPLTFAHSTPLGGTALQW 430
 58 371 tfealittfmflhrttdlkwlitls slfaapntrkrtltpvaiinpltpahstplggtaalqw 430
 59 434 GIAQWQWQSKRPDYNQMPFACLNQSHALISPLDITMKRQYFLVSLKPTPTSKVRQLDI 493
 60 GIAQWQWQSKRPDYNQMPFACLNQSHALISPLDITMKRQYFLVSLKPTPTSKVRQLDI 493
 61 434 giawqwqwskrpdynqmpfaclnqshalispdltmkrqyflvslkptptskvrqlidi 493
 62 494 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 540
 63 TQKRAKRRHSYSYAVITWEVLSKKQFEEAVNPLQIMYSVSGRRIVNHESLEYL 540
 64 494 ptkrakrrhsysyavitwevlskkqfeeavnplqimysvsgrrivnhesleyl 540

RESULT 11
 AAB58948
 1 AAB58948 standard: Protein: 154 AA.
 2
 3 AAB58948;
 4
 5 27 MAR 2001 (first entry)
 6
 7

DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 646.

XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neotropic; neurprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antifungal; vulvaric; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.

XX Homo sapiens.

XX W0200055172-11

XX 21 SEP 2000

XX 08-MAR-2000; 2000WO-0205881.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC

XX Rosen CA, Rubin SM.

XX WPI; 2000-41515758

XX N-PSDB; AAF21841.

XX New human breast and ovarian cancer associated gene sequences and the
XX polypeptides encoded by these genes, useful in the prevention,
XX treatment and diagnosis of cancer, immune disorders, cardiovascular
XX disorders and neurological diseases -

XX Claim 11; Page 1086; 1299pp; English.

XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
XX proteins AAF22711 - AAF25912. The DNA and protein sequences are
XX associated with breast and ovarian cancer. Included in the invention are
XX sequences AAF22832 - AAF22840 and AAF25912 which are used in the
XX isolation and characterization of the DNA and protein sequences of the
XX invention. The breast and ovarian cancer associated DNA, protein, agonist
XX or antagonist sequences exhibit cytostatic; immunosuppressive;
XX neotropic; neurprotective; antiviral; antiallergic; hepatotropic;
XX antidiabetic; antiinflammatory; antifungal; vulvaric; anticonvulsant;
XX antibacterial; antifungal; antiparasitic and cardiant activity. The
XX polynucleotide and protein sequences are used in the diagnosis of cancer,
XX particularly breast and ovarian cancer. The nucleic acid sequences,
XX proteins, agonists and antagonists may also be used in the diagnosis,
XX prevention and treatment of immune disorders e.g. Addison's disease,
XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
XX arthritis and ulcerative colitis; cardiovascular disorders such as
XX myocardial ischaemia; wound healing; neurological diseases such as
XX cerebral anoxia and epilepsy; and infectious diseases

XX Sequence 153 AA.

Query Match 21.3% Score 126 DB 21 Length 153
Best local Similarity 100.0% Prod. No 340-121
Matches 126 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Oy 97 YMDNENI NPI IERTFYDVAWNI PPRPI DEIAT CANV I DMTPI RUKIKTNGI LUN 154
Db 1 ymdnensilnkrtktydvwplrfilheialgnyihmtpplihdiktngilldn 60

Oy 157 PPRVPIATPISKRNEMSI QPRKSTALSDPI IYMHV NYHITKSFARIKH IYSYA 210
Db 61 PPRVPIATPISKRNEMSI QPRKSTALSDPI IYMHV NYHITKSFARIKH IYSYA 120

Oy 217 VITREY 222

Db 121 vitrey 126

RESULT 12

AAM25501

ID AAM25501 standard; Protein, 112 AA

XX AAM25501;

XX 16 OCT 2001 (first entry)

XX Human protein sequence SEQ ID No:1016.

XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti HIV; fungicide; antimutagen; cardiocascular; antianemic; anemia;
KW antiagregant; haemostatic; vulvaric; antifungal; osteopathic; eczema;
KW dermatological; antiallergic; antinflammatory; antidiabetic; cytostatic;
KW neurprotective; antidepressant; neotropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antiamphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.

XX Homo sapiens

XX W020015455 A2.

XX 26-JUL-2001.

XX 22 DEC 2000, 2000WO 0545017.

XX 22 DEC 1999, 99US 0171275.

XX 21-JAN-2000, 2000US 048725.

XX 25 APR 2000, 2000US 052447.

XX (HSL) HSL010R.

XX Tang Yi, Liu C, Guzman RT.

XX WPI; 2001-457603/49.

XX N-PSDB; AAH99442.

XX Isolated human polynucleotides encoding polypeptides useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

XX Claim 20; Page 269; 1217pp; English.

XX AAM25912 to AAM26001 encode the human proteins given in AAM25925 to
XX AAM25962. The proteins are have activities based on the tissues and
XX cells they are expressed in, such as: antiinflammatory; antirheumatic;
XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
XX central nervous system; virucide; anti HIV; fungicide; antimutagen;
XX cardiovascular; antianemic; antiagregant; haemostatic; vulvaric;
XX antifungal; osteopathic; dermatological; antiallergic; antinflammatory;
XX antidiabetic; cytostatic; neurprotective; antidepressant; neotropic;
XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides
XX encoding them can be used in gene therapy, antisense therapy and vaccine
XX production. The proteins and polynucleotides are useful for screening for
XX agonists or antagonists of a protein and for the treatment and diagnosis
XX of disorders associated with the activity of a protein e.g. inflammation,
XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
XX infections, autoimmunity, genetic diseases, haematopoietic disorders,
XX anemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
XX osteoporosis, severe combined immunodeficiency, eczema, allergic
XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
XX Alzheimer's disease, Parkinson's disease, neurodegenerative and
XX neurological disorders.

PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249267.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249301.
 PR 01-DEC-2000; 2000US-0250310.
 PR 01-DEC-2000; 2000US-0250351.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251090.
 PR 05-DEC-2000; 2000US-0251610.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254007.
 PR 05-JAN-2001; 2001US-0254678.
 XX
 PA (HUMAN) HUMAN GENOME SCI INC.
 XX
 PT Rosen CA, Barish SC, Ruben SM;
 XX
 DR WPI: 2001-165460/50.
 DR N-PSDB: AAS27152
 XX
 PT Novel polypeptides useful for diagnosing, treating, preventing and/or
 PI prognosing disorders related to the proteins, including cancers, immune
 PI disorders and neuronal disorders.
 XX
 PS Claim 1: SEQ ID No 800; PR0pp; Englist
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II), (II), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejection and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorder, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anemia), myeloproliferative
 CC disorders, primary hematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumor proliferation in pathologies (e.g. acquired immune deficiency
 CC syndrome (AIDS)). AA017050-AA017492 represent novel signal transduction
 CC pathway protein amino acid sequences of the invention
 XX
 Query Match: 1.0%; Score 10; Ids 22; Length 167;
 Best Local Similarity: 100.0%; Pred. Id: 0.1;
 Matches: 10; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

cy 146 EIKTQHLLD 155
 1111111111
 DB 4 EIKTQHLLD 155

RESUME 14
 AA017241
 ID AA017241 standard, Protein, 254 AA.
 XX
 A7 AA017241:
 XX
 LI 07 MAY 2001 (first entry)
 XX
 DE Novel signal transduction pathway protein, seq ID 800.
 XX
 KW B-cell leukemia, lymphoma, hematological, immune suppressive, tumour;
 KW anti-inflammatory; anti-HIV; antibacterial; anti-inflammatory; cancer;
 KW immune system disorder, rheumatoid arthritis, inflammatory condition;
 KW organ transplant rejection, infection, hepatitis C, blood disorder;
 KW sickle cell anemia; hyperproliferative disorder; Gaucher's disease;
 KW neurodegenerative disorder, Alzheimer's disease, Parkinson's disease;
 KW chromosomal abnormality, Down syndrome, ischaemic renal disorder;
 KW cardiovascular, respiratory, wound healing, endocrine, Addison's disease,
 KW reproductive system, gastrointestinal, liver disorder; AIDS;
 KW acquired immune deficiency syndrome.
 XX
 OS Homo sapiens
 XX
 IN W200104715 AL
 XX
 PD 02 AUG 2001.
 XX
 FI 17 JAN 2001; 2001US01412.
 XX
 PR 31-JAN-2000; 2000US-0179055.
 PR 01-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0185150.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0196123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0226213.
 PR 14-AUG-2000; 2000US-0226214.
 PR 14-AUG-2000; 2000US-0227266.
 PR 14-AUG-2000; 2000US-0227267.
 PR 14-AUG-2000; 2000US-0227268.
 PR 14-AUG-2000; 2000US-0227270.
 PR 14-AUG-2000; 2000US-0227447.
 PR 14-AUG-2000; 2000US-0227577.
 PR 14-AUG-2000; 2000US-0227578.
 PR 14-AUG-2000; 2000US-0227579.
 PR 18-AUG-2000; 2000US-0228279.
 PR 22-AUG-2000; 2000US-0228581.
 PR 22-AUG-2000; 2000US-0228668.
 PR 22-AUG-2000; 2000US-0227182.
 PR 24-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.

PR	17-N-V-2000;	200008-0249214.
PR	17-N-V-2000;	200008-0249215.
PR	17-N-V-2000;	200008-0249216.
PR	17-N-V-2000;	200008-0249217.
PR	17-N-V-2000;	200008-0249218.
PR	17-N-V-2000;	200008-0249244.
PR	17-N-V-2000;	200008-0249245.
PR	17-N-V-2000;	200008-0249260.
PR	17-N-V-2000;	200008-0249265.
PR	17-N-V-2000;	200008-0249297.
PR	17-N-V-2000;	200008-0249298.
PR	17-N-V-2000;	200008-0249300.
PR	01-1037-2000;	200008-0250160.
PR	01-1037-2000;	200008-0250191.
PR	05-1037-2000;	200008-0251000.
PR	05-1037-2000;	200008-0251088.
PR	05-1037-2000;	200008-0251671.
PR	08-1037-2000;	200008-0251479.
PR	08-1037-2000;	200008-0251856.
PR	08-1037-2000;	200008-0251868.
PR	08-1037-2000;	200008-0251869.
PR	08-1037-2000;	200008-0251989.
PR	08-1037-2000;	200008-0251990.
PR	11-1401-2000;	200008-0254097.
PR	05-JAN-2001;	200101-0259678.

XX

XX

112

XX

XX

XX

[11]

XX

Busb. Local Similarity Index; Prod. No. 013

[illegible]

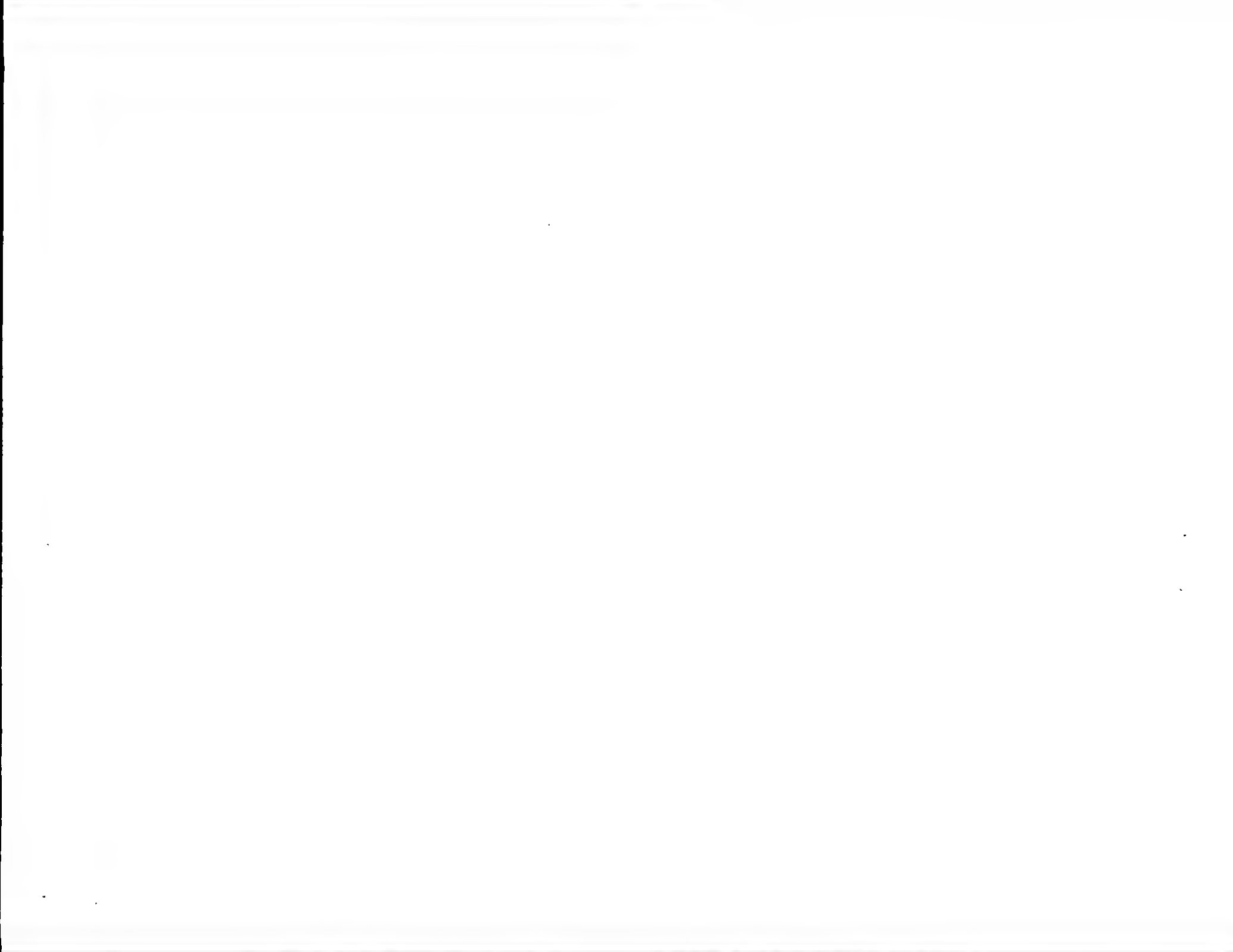
RESUME 15

AAB85048
 ID AAB85048 standard; Protein: 330 AA
 XX
 AC AAB85048;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE Human SER4 protein sequence.
 XX
 KW Serine/threonine kinase-like protein; SERX; breast; testicular; cancer;
 KW cardiac arrest; autoimmune disorder; cytostatic; cardiac gene therapy
 KW immunosuppressive; antiasthmatic; antifibrinolytic; SER4.
 XX
 OS Homo sapiens.
 XX
 PN W0200136645-A2.
 XX
 PD 25-MAY-2001.
 XX
 PE 17 NOV 2000; 2000WO-0531744.
 XX
 PR 17-NOV-1999; 99US-0165986.
 PR 09-FEB-2000; 2000US-0181447.
 PR 03-APR-2000; 2000US-0194195.
 PR 05-APR-2000; 2000US-0194839.
 PR 07-APR-2000; 2000US-0195647.
 PR 13-APR-2000; 2000US-0197080.
 PR 15-SEP-2000; 2000US-0232677.
 PR 16-NOV-2000; 2000US-0165986.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Quinn KE, Spyttek KA, Majumder K, Verritt C, Burgess C, Fernandes E;
 PI Taupier R, Bastelli L, Herrmann JL;
 XX
 DR WP1; 2001-4:6006/35.
 DR N-PSDB; AAF63969.
 XX
 FI New isolated SERX polynucleotides and polypeptides related to the
 FI serine/threonine kinase family of proteins, useful for determining and
 FI treating diseases related to altered levels of the polypeptide -
 XX
 PS Claim 1; Page 21, 127pp; English.
 XX
 CC The invention relates to serine/threonine kinase-like proteins, termed
 CC SERX. The SERX polynucleotides can be used to express SERX protein (e.g.,
 CC viral vector-mediated expression vector in a host cell in gene therapy
 CC applications), to detect SERX mRNA (e.g., in a biological sample) or a
 CC genetic lesion in a SERX gene and modulate SERX activity. The SERX
 CC polypeptides, polynucleotides, antibodies can also be used to treat or
 CC prevent a pathology associated with SERX. Disorders associated with
 CC aberrant SERX expression or activity include breast or testicular cancer,
 CC cardiovascular defect, autoimmune disorders and asthma. Disorders
 CC associated with aberrant SERX expression include, blood clotting
 CC hematopoietic and tumor related disorders. The present sequence
 CC represents the amino acid sequence of human SER4 protein.
 XX
 SO Sequence 330 AA;

Query Match 148; Score 10; DB 22; length 330;
 Best Local Similarity 100.0%; Pred No 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 DIKIQNILLD 155
 IIIIIIIIII
 Db 128 DIKIQNILLD 137

Search completed: May 13, 2002, 21:32:38
 Job time: 8628 sec



GenCore version 1.5
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OM nucleic - nucleic search, using SW model

Run on: May 13, 2002, 18:55:39, Search time 2937.39 Seconds
(without alignments)
9640.059 Million cell updates/sec

Title: US-09-445-223-2
Perfect score: 2098
Sequence: 1 ggcattatggatggatggg aaaaaaaaaaaaaaaaaa 2098

Scoring table: G100_NUC
Gapop 60.0, Gapext 60.0

Searched: 13736707 seqs, 6748477512 residues

Word size: 1

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_low:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	692	32.2	811	10	BC170405 6024227461
2	656	31.0	883	10	BC170405 602411943
3	650	31.0	883	10	BC170405 602411943
4	598	28.5	1011	10	BM469352 AGENCOURT
5	592	28.2	500	9	AT1746575
6	554	26.4	636	10	BE551615 74124061
7	551	26.3	912	10	BE551615 74124061
8	532	25.4	616	9	AA160647 3149811
9	520	25.4	642	9	AW960501 EST722572
10	505	24.1	879	10	BE877822 601486392
11	500	23.9	759	10	BE877822 601486392
12	455	21.7	606	9	AW960501 EST722572
13	449	21.4	455	9	AA160647 3149811
14	448	21.4	835	10	BE877822 601486392
15	445	21.2	828	10	BE877822 601486392
16	421	20.2	616	9	AA160647 3149811
17	423	20.2	422	9	AA574167

c 18	422	20.1	516	9	AW593657	AW593657 x194307.x
c 19	422	20.1	511	9	AW150819	AW150819 xq39168.x
c 20	412	19.5	891	10	BM010110	BM010110 602411943
c 21	411	19.6	483	9	A1343247	A1343247 tb94a04.x
c 22	401	19.2	445	9	AW820715	AW820715 RC5-ST030
c 23	394	18.8	100	9	AA825052	AA825052 od60b09.x
c 24	393	18.7	487	9	AW393452	AW393452 RC5-ST030
c 25	391	18.6	1056	10	BM468817	BM468817 AGENCOURT
c 26	387	18.4	776	10	BC574192	BC574192 602596077
c 27	386	18.4	742	10	BE1225743	BE1225743 602851345
c 28	381	18.2	121	10	BE062840	BE062840 7b70q03.x
c 29	371	17.7	1112	10	BE125423	BE125423 601763549
c 30	370	17.6	446	9	BE002713	BE002713 QV4-BN009
c 31	355	16.9	476	9	AA913804	AA913804 ol35d11.s
c 32	355	16.9	616	9	A1307810	A1307810 tb28d07.x
c 33	353	16.8	445	9	AW820730	AW820730 RC5-ST030
c 34	350	16.7	350	10	BE754627	BE754627 QV3-CT055
c 35	350	16.7	122	9	AA722537	AA722537 qd73q08.x
c 36	349	16.6	418	9	A1409817	A1409817 tm92103.x
c 37	348	16.6	439	9	A1360934	A1360934 tb20c05.x
c 38	346	16.5	446	9	AW385642	AW385642 PM0-LT003
c 39	341	16.3	166	9	AW293431	AW293431 RC5-ST030
c 40	341	16.3	945	10	BE758079	BE758079 602020940
c 41	333	15.9	446	9	AW610171	AW610171 RC5-ST030
c 42	331	15.8	616	10	BE669380	BE669380 602295259
c 43	325	15.5	429	9	AA158366	AA158366 ERT2p4131
c 44	322	15.3	777	10	BE1818703	BE1818703 603047520
c 45	319	15.2	483	10	CU58866	CU58866 CU58866 Huma

ALIGNMENTS

RESULT 1
BC170405
LOCUS BC170405 811 bp mRNA linear EST 06-FEB-2001
DEFINITION 6024227461 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4426016 5', mRNA sequence.
ACCESSION BC170405
VERSION BC170405.1 GI:12677108
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 811)
REFERENCE
AUTHOR NIH MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rstraus@nigms.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the MGC website: <http://www.mgc.ac.uk>
Placer: LLAM10172 row: 4 column: 09
High quality sequence step: 731.
FEATURES
source
Location/Qualifiers
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/organism "Homo sapiens"
/clone "IMAGE:4426016"
/clone "IMAGE:4426016"
/clone "NIH_MGC_89"
/tissue_type "hyperplasia, cell line"
/lab_host "BUDOP (phage resistant)"
/vector "pUC19 (phage resistant)"
/site "5' end: closed unidirectionally; oligo-dT primed.
Average insert size 1.2 kb. Library enriched for full length clones and cDNA stability Life Technologies.
Note: This is a NIH_MGC Library."

TABLE 1. Continued. List of Species of Birds, Mammals, Reptiles, Fish, and Amphibians (continued)

1619 unnt unnt laurcaulxcl agal unnt lrl glry aggnarl lual al quaqyqat. 1628

Db 541 GGCCTGGCTTAACAGAGCGGTAGATGCCCCTCTGTCAGGAGCTTATCATGAAAGAGGAC 600

QY 1679 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1704

Db 601 TATGAAGCTTTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 650

RESULT 3
 BM469352
 LOCUS 884 bp mRNA linear EST 12-MAR-2001
 DEFINITION mRNA sequence.
 ACCESSION BM469352
 VERSION BM469352.1 GI:13286999
 KEYWORDS EST
 SOURCE Human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 884)
 AUTHOR NIAH MGC (http://www.ncbi.nlm.nih.gov)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rstraub@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incode Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at
 http://image.llnl.gov
 Plate: LLAM10471 row: c column: 12
 High quality sequence stop: 767.

FEATURES
 source Location/Qualifiers
 1..883
 /organism "Homo sapiens"
 /db_xref "taxon:9606"
 /clone "IMAGE:4540787"
 /clone_lib "NIH_MGC_92"
 /tissue_type "embryonal carcinoma, cell line"
 /lab_host "DH10B (phage-resistant)"
 /note "Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 192 a 196 c 164 g 210 t 1 others
 ORIGIN

Query Match: 31.0%; Score 650; DB 10; Length 884;
 Best Local Similarity: 100.0%; Pred. No. 4e+141;
 Matches: 650 Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1267 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1326

Db 1 TGTAAAT 60

QY 1327 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1386

Db 61 TGTAAAT 120

QY 1387 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1446

Db 121 TGTAAAT 240

QY 1447 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1506

Db 181 TGTAAAT 240

QY 1507 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1566

Db 241 AGCAATAATAAAATATATATATATATATATATATATATATATATATATAT 300

QY 1567 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1626

Db 401 TGTAAAT 460

QY 1627 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1686

Db 461 TGTAAAT 420

QY 1747 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1806

Db 481 TGTAAAT 540

QY 1807 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1866

Db 541 TGTAAAT 600

QY 1867 TATTAAGTCTTATACCAAGGATAGAAAGAGCTTATCAATGAAATATGAA 1926

Db 601 TGTAAAT 660

RESULT 4
 BM469352
 LOCUS 1011 bp mRNA linear EST 05-FEB-2002
 DEFINITION mRNA sequence.
 ACCESSION BM469352
 VERSION BM469352.1 GI:18518494
 KEYWORDS EST
 SOURCE Human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1011)
 AUTHOR NIAH MGC (http://www.ncbi.nlm.nih.gov)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rstraub@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at
 http://image.llnl.gov
 Plate: LLAM12451 row: e column: 05
 High quality sequence stop: 663.

FEATURES
 source Location/Qualifiers
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 /organism "Homo sapiens"
 /db_xref "taxon:9606"
 /clone "IMAGE:5585260"
 /clone_lib "NIH_MGC_92"
 /tissue_type "embryonal carcinoma, cell line"
 /lab_host "DH10B (phage-resistant)"
 /note "Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 219 a 275 c 254 g 233 t
 ORIGIN

Query Match: 28.5%; Score 598; DB 10; Length 1011;


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RESULT 10
HEB77822
LOCUS BEB77822 870 bp mirna linear EST 20 OCT 2000
DEFINITION 601486392F1 NIH_MGC_h5 Homo sapiens cRNA clone IMAGE:3888815.5,
mirna sequence.
ACCESSION BEB77822
VERSION BEB77822.1 GI:19436548

```

Q1 1638 q1wqetqat acout lrtgt rcaqg 1657


```

RESULT 13
AI343850/c
LOCUS
DEFINITION
  AI343850
  455 bp. mRNA linear. EST 02 FEB 1999
  J070781.x1 NCI_CGAP_K195 Homo sapiens cDNA clone IMAGE:191713 3'.
  mRNA sequence.
ACCESSION
  AI343850
  AI343850.1 GI:4081056
VERSION
  EST
KEYWORDS
  human.
SOURCE
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Eumetazoa; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1. (bases 1 to 455)
  NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
TITLE
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs@mail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. E. Soto-Scares, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E.R. Consortium/LEND at.

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Qy	1481	gagcagacagagcgcctctatgctctcttcagcaataataatctatctctcagcagcaggaac	1540
Db	455	GATGACAAGATCACTCCATGCTCTTCAGCAATAAATAAATCCACCTCAACTGCAAGAAAC	396
Qy	1541	tcaggaacgcttttcagcgttgggtatagtcacagcagctggatccagagcgaaggggaaqatatt	1600
Db	395	TCAGAACGCTCTTCAGCCTGGTATTACCCGAGCAGTGTATTCAGAGCAAAAGCTAAGATATT	336
Qy	1601	gtgaagcccaal-garaggaagcgttcgcttaacacagatctctcaatgacgctttctctcaggaac	1660
Db	334	GTGAAACCAATGACAGCAAGCTCTGGCTTAACAGTGTCTAGATGGCTTTCTCTCAGGAGC	276
Qy	1661	ttgatctatgaagagagatctatgaacttctttatgctaraggaagctatcaaggaatctcaaggaatc	1720
Db	275	TTGATCATGAAGAGGATATGAACCTTGTTACTACCAAGCTTACAGAGGACTCAAAAGTG	216
Qy	1721	agagaaattactagacattactgcacatctcagagcaggaagattttgctgaagcttatagtcaga	1780
Db	215	AGACATATTATACGACATATTCACATCTCAAGGAAAGAAATTTGCCAAGCTTATAGTACAA	156
Qy	1781	gaatttgaagagctcagcaagcaggaatggagctttcagccttgcagaggaagatttctgatttttt	1840
Db	155	AAATTGAAGACATAACCAACAATGGCTTTCAGTCTTACCTTGAGAAATCTGTGGTCTCT	96
Qy	1841	agattacacatcttcaattttatctcaaaatcaaaagcatctcaagtcacttttctcaagaa	1900
Db	95	AGATCACATATTCTAAATTTACTTCAAAATAAAGCATGTAAGTCACTGTTTTTCAAGAA	46
Qy	1901	gaattatgtttttatgaagggatatttata	1924
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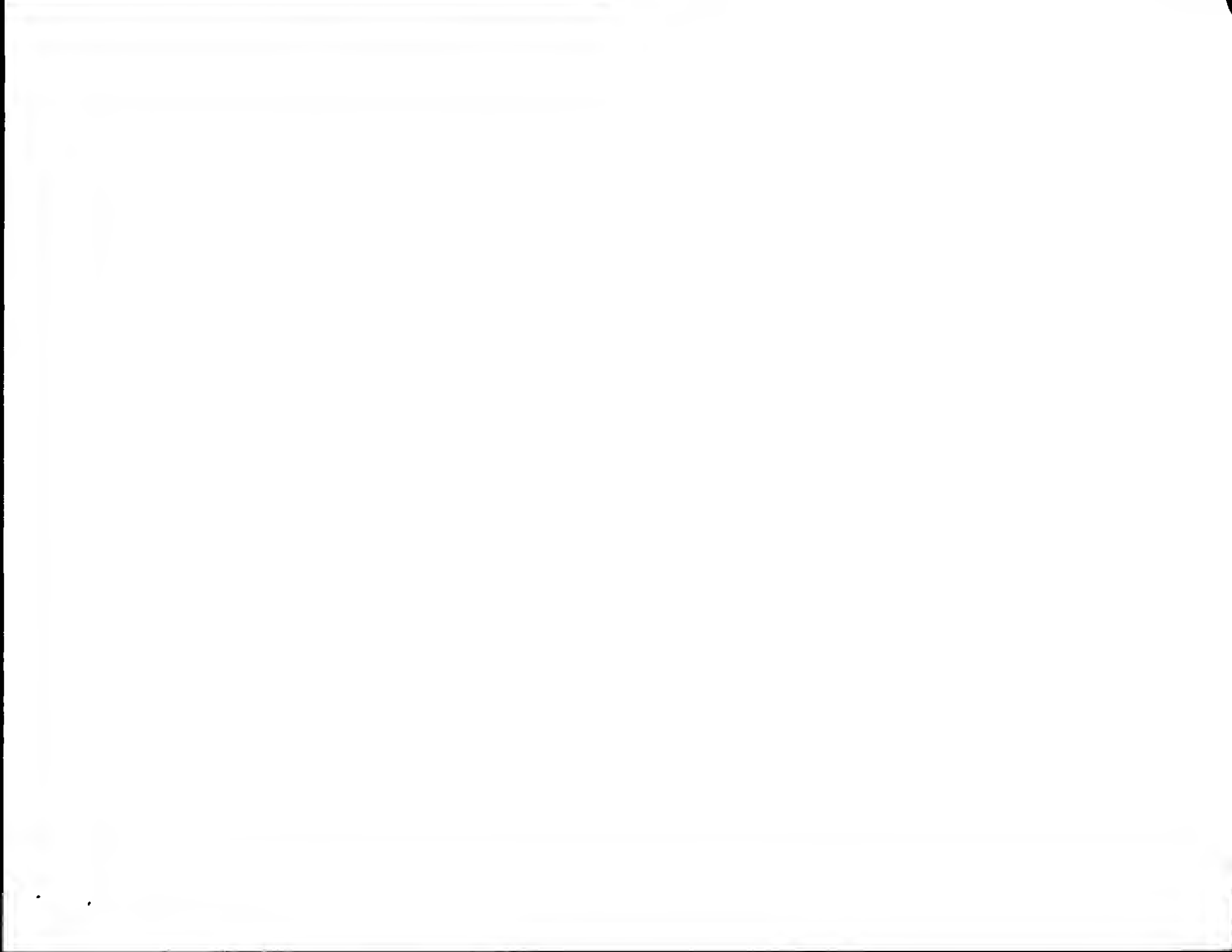
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RESULT 14
BI820776
LOCUS      B1820776               675 bp     mRNA             linear     RF1 04-007-2001
DEFINITION Homo sapiens CDNA clone IMAGE:5175690.5',
            mRNA sequence.
ACCESSION  BI820776
VERSION    BI820776.1  GI:15932326
KEYWORDS   EST.
SOURCE     human.
            ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;

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[illegible][illegible]

Search completed: May 13, 2002, 19:58:11
Job time: 3752 sec



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Query Match      97.5%   Score 1668;   ID #:   Length 1931;
Best local Similarity 97.0%   Prev. No 0;
Matches 1938, Conservation 0; Mismatches 4; Indels 0; Gaps 0
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RESULT 4
DS-09-069-123 2
; Sequence 2, Application of DS/09069023A
; Patent No. 648573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel

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RESULT 5
 HS-08-700 575-31
 : Sequence 31, April 11, 2008, HS/08700575
 : Patent No. 5817479

```

RESUL1 7
US 09 054-298-7
: Sequence 7. Application: US/09054298
: Patent No. 6136953
: GENERAL INFORMATION:
: APPLICANT: Lee, Mei En
: APPLICANT: Haber, Eshar
: APPLICANT: Jain, Mukesh
: APPLICANT: Yeh, Shaw Fang
: TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
: NUMBER OF SEQUENCES 40
: CORRESPONDENCE ADDRESS:
: ADPESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0d
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 09/054,298
: FILING DATE: 02 APR 1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/616,368

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1: INFORMATION FOR SEQ ID NO. 1
2:     SEQUENCE CHARACTERISTICS:
3:         LENGTH: 700 base pairs
4:         TYPE: NUCLEOTIDE
5:         STRAIN: B1
6:         ORGANISM: Homo sapiens
7:         TOPOLOGY: linear
8:         MOLECULE TYPE: DNA
9:         HYPOTHEICAL: NO
10:        ANTI-SENSE: NO
11:        ORIGINAL SOURCE:
12:            ORGANISM: Homo sapiens
13:            IMMEDIATE SOURCE:
14:            IS: 07-846-002-1

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: CURRENT FILING DATE: 1998-08-04
: EARLIER APPLICATION NUMBER: 68/2045,157
: EARLIER FILING DATE: 1998-08-07
: NUMBER OF SEQ. IDS: 8
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 7812
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(6879)
: NAME/KEY: cdsinit
: LOCATION: (100)...(102)
: NAME/KEY: cdsinit
: LOCATION: (102)...(102)
: NAME/KEY: cdsinit
: LOCATION: (226)...(226)
US-09-468-592

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Query Match 1.7%, Same 36, ID 1, Length 7812,
Best Local Similarity 100.0%, Prod. No. 11e-16,
Matches 10, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

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QY 2063 1111111111111111111111111111111111 2098
DB 7768 1111111111111111111111111111111111 7803

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```

RESULT 14
US-09-592-891A-8
: Sequence 3, Application US/09592891A
: Patent No. 6329174
: GENERAL INFORMATION:
: APPLICANT: Xiao-Xhou Michelle Wang
: APPLICANT: Xavier Georges Sarda
: APPLICANT: Michael David Tamalski
: APPLICANT: Vincent Paul Mary Wiorate
: TITLE OF INVENTION: Heliothis glutamate Receptor
: FILE REFERENCE: A32815 072667.0118
: CURRENT APPLICATION NUMBER US/09592891A
: CURRENT FILING DATE: 2000-01-22
: NUMBER OF SEQ. IDS: 14
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 8
: LENGTH: 1052
: TYPE: DNA
: ORGANISM: Heliothis virescens
US-09-592-891A-8

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Best Local Similarity 100.0%, Prod. No. 6e-06,
Matches 45, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

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QY 2064 1111111111111111111111111111111111 2098
DB 1017 1111111111111111111111111111111111 1051

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RESULT 14
US-09-412-102-3
: Sequence 3, Application US/09412102
: Patent No. 6228992
: GENERAL INFORMATION:
: APPLICANT: JESSEN, HOLLY J
: APPLICANT: MEYER, JERRY E
: TITLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
: TITLE OF INVENTION: NEMATODES IN PLANTS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)

```

```

: STREET: 4605 Glenwood Ave., Suite 310
: CITY: Raleigh
: STATE: NC
: COUNTRY: US
: ZIP: 27622
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.0
: CLASSIFICATION DATA:
: APPLICATION NUMBER: 09/217,787
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/217,787
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Spruill, W. Murray
: REGISTRATION NUMBER: 62,944
: REFERENCE NUMBER: 5718-180
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-420-2202
: TELEFAX: 919-811-0170
: INFORMATION FOR SEQ ID NO 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1325 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: topology: linear
: MOLECULE TYPE: cDNA
: ORIGINAL SOURCE:
: ORGANISM: Pea weevils
: IMMEDIATE SOURCE:
: CLONE: p52218
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 129..583
US-09-412-102-3

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Query Match 1.7%, Same 35, ID 1, Length 1325,
Best Local Similarity 100.0%, Prod. No. 6.0e-06,
Matches 35, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

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QY 2064 1111111111111111111111111111111111 2098
DB 1236 1111111111111111111111111111111111 1344

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```

RESULT 14
US-09-217-787-3
: Sequence 3, Application US/09217787
: Patent No. 6284948
: GENERAL INFORMATION:
: APPLICANT: JESSEN, HOLLY J
: APPLICANT: MEYER, JERRY E
: TITLE OF INVENTION: GENES AND METHODS FOR CONTROL OF
: TITLE OF INVENTION: NEMATODES IN PLANTS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
: STREET: 4605 Glenwood Ave., Suite 310
: CITY: Raleigh
: STATE: NC
: COUNTRY: US
: ZIP: 27622
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:

```

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his help in preparing this paper.